

	FEATURES	source	Location/Qualifiers
	1 .975	/organism="Homo sapiens"	
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:6381368"		
	/tissue="Type=carcinoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_id="NIH_MGC_40"		
	/note="Organ: prostate; Vector: pORN7; Site_1: Xhol;"		
	Site 2: EcoRI; cDNA made by oligo-dT priming.		
	Directionally cloned into EcoRI/Xhol sites using the		
	following 5' adaptor: GGGAG(G). Library constructed by		
	Ling Hong in the laboratory of Gerald M. Rubin (University		
	of California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies).		
	Note: This is a NIH_MGC Library."		
ORIGIN			
	Query Match Score 512; DB 5; Length 975;		
	Best Local Similarity 95.1%; Pred. No. 5 4e-115;		
	Matches 557; Conservative 0; Mismatches 26; Indels 3; Gaps 3;		
Qy	1 GCGNCCGGNNNGNGCAAGGTGCTGAGGCCCTTAGNCCTCCCTGCCCTCCCTGCCCTCC 60		
Db	189 GCGGCCGGCGCTGGCCAGGTGCTGAGGCCCTTAGNCCTCCCTGCCCTCCCTGCCCTCC 248		
Qy	61 TCTGCCGGCGTACATGGGTGGTAGATGGCTCCGA-CGGGA 119		
Db	249 CCTGCCGGCGAGGTGCTGAGGCCCTTAGNCCTCCCTGCCCTCCCTGCCCTCC 308		
Qy	120 GGCGCGGCTGCTGATGCCGCTGGCGAGAAGCGCCATTCCAGTCAGCTGCCCTCC 179		
Db	309 GGCGCGGCTGATGCCGCTGGCGAGAAGCGCCATTCCAGTCAGCTGCCCTCC 368		
Qy	180 CC-GGCGCACTTGCGAGTCCCCTCCGAGCAGGACCGC 238		
Db	369 CGGACGCCCTCGAGATCCCCGGTTAACCTGGACAGCACCGC 428		
Qy	239 CCTCCCTCTGAGCCGATGCCGAGCCAGCGCCAGGCTCCCT 298		
Db	429 CCTCCCTCTGAGCCGAGCCAGGCTCCCT 488		
Qy	299 TCTCCCTGTTGGATCCCTAGACCACAGCTCAGGCCAGAACAGCTGAACT 358		
Db	489 TCTCTGTTGGATCCCTAGACCACAGCTCAGGCCAGAACAGCTGAACT 548		
Qy	359 CATTGGCACATACCGCCATGTTGACCGTCCACCGGCCAGGTGCTAACCTGTGACAATG 418		
Db	549 CATTGGCACATACCGCCATGTTGACCGTCCACCGGCCAGGTGCTAACCTGTGACAATG 608		
Qy	419 TCCAGGAGGAACCTPATGTTCTGAGCATGTTGACCAACAAAGCTGCCGCTCTGAG 478		
Db	609 TCCAGGAGGAACCTPATGTTCTGAGCATGTTGACCAACAAAGCTGCCGCTCTGAG 668		
Qy	479 TTGCCCTGTGGGACCTTACCAAGCTGAAATGCAATGAGAATGCTGATG 538		
Db	669 TGCCCTGTGGGACCTTACCAAGCTGAAATGCAATGAGAATGCTGATG 728		
Qy	539 TCAGCCATGCCATGCCATGTTGAGAAATTACCTTGTC 580		
Db	729 TCAGCAATGCCATGCCATGAGAATTAACCTTGTC 770		
RESULT 2			
BQ927810	975 bp	mRNA	linear EST 20-AUG-2002
LOCUS			
DEFINITION	5' mRNA sequence.		
ACCESSION	BQ927810		
VERSION	1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	NIH-MGC http://mgc.ncbi.nih.gov/		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgabbs@mail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://ilnl.nih.gov Plate: LCM571 row: p column: 17 High quality sequence stop: 498.		
RESULT 3			
BQ88267	882 bp	mRNA	linear EST 15-JUL-2002
LOCUS	BQ688267_8047240 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207591		
DEFINITION	5' mRNA Sequence.		
ACCESSION	BQ688267		
VERSION	1		
KEYWORDS	EST.		
SOURCE			
ORGANISM			
REFERENCE	TCAGCCATGCCATGGCCAATATGAGAAATTACCTTGTC 584		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgabbs@mail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://ilnl.nih.gov Plate: LCM571 row: p column: 17 High quality sequence stop: 498.		

ORGANISM	Homo sapiens	QY	536 TAGTCAGCCATGCCCATGGCCAATGAGAAATTACCTTGTCTGCC	584
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 882)	Db	526 bp mRNA Homo sapiens cDNA clone IMAGE:1702349 3,	
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	RESULT 4	BF433925	
JOURNAL	Unpublished (1999)	LOCUS DEFINITION	7q56q17.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:1702349 3,	
COMMENT	Contact: Robert Straussberg, Ph.D.	similar to TR:075505 O75505 TNFR-RELATED DEATH RECEPTOR-6.		
Tissue Procurement: ATCC		/contains MER22.t2 PTRS repetitive element ; mRNA sequence.		
cDNA Library Preparation: Rubin Laboratory				
CDNA Library Arrayed by: The I.M.A.G.E. Consortium		ACCESSION	BF433925	
DNA Sequencing by: Agencourt Bioscience Corporation		VERSION	BF433925.1 GI:11446056	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:		KEYWORDS	EST.	
http://image.llnl.gov .		SOURCE	Homo sapiens (human)	
Plate: ULCM363 row: 0 column: 16		ORGANISM	Homo sapiens	
High quality sequence stop: 689.		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Source	1..882	COMMENT	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
FEATURES	/organism="Homo sapiens"	REFERENCE	1.. (bases 1 to 526)	
Source	/mol type="mRNA"	AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
	/db_xref="taxon:9606"	TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index.	
	/clone=IMAGE:1620591"	JOURNAL	Unpublished (1997)	
	/issue type="ductal carcinoma, cell line"	COMMENT	Contact: Robert Strausberg, Ph.D.	
	/lab_ho= "DH10B (phage-resistant)"		Email: cgaps-b@mail.nih.gov	
	/clone lib="NIH MGC_110"		Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.	
	/note="Organ: pancreas; Vector: pOTB7; Site 1: XbaI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcorI/XbaI sites using the following 5' adaptor: GGCACCGAG (G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH-MGC Library."		CDNA Library Preparation: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.	
ORIGIN			DNA Sequencing by: Washington University Genome Sequencing Center	
			Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov	
			Seq primer: -401P from Gibco High quality sequence stop: 427.	
			Location/Qualifiers	
			1..526	
			/organism="Homo sapiens"	
			/mol type="mRNA"	
			/db_xref="taxon:9606"	
			/clone="IMAGE:1702349"	
			/tissue type="carcinoid"	
			/lab_host="DH10B"	
			/clone_lib="NCI-CGAP Lu24"	
			/note="Organ: lung; Vector: pTT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP Lu24 was prepared, and ss circles were made in vitro. Following HPLC purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bentso Soares and M. Patima Bonaldo."	
		FEATURES		
		Source		
Query Match	85.4%	Score 498.6; DB 5; Length 882;		
Best Local Similarity	98.9%	Pred. No. 1e-111; 4; Gaps 2;		
Matches	523;	Conservative 0; Mismatches 4; Indels 2; Gaps 2;		
QY				
Db				
Query	58	TCCTCTGCCCCCTTAGAGTGCACATGGCGCTCCGG-CCG 116		
Db	1	TCCTCTGCCCCCGCAGCTGGCATGGGTAGATGGCTCCGGCCG 60		
QY	117	GGAGCGGCCGCTGGATGCGCTGGAGCGATGGCGACTCTCCAGCACAGCA 176		
Db	61	GGAGCGGCCGCTGGATGCGCTGGAGCGATGGCGACTCTCCAGCACAGCA 120		
QY	177	GCCCCC-GGCCAACCTTGAGCTCCGGTAGCCAGTGGGACCTCTCCAGCACAGCA 235		
Db	121	GCCCCGGCCCTCTGAGCTCCGGTAGCCAGTGGGACCTCTCCAGCACAGCA 180		
QY	236	CGCCCTCGCTCTGAGGCCATGCCAGGCCAGCAAGATGCCAGTGGGCTC 295		
Db	181	CGCCCTCGCTCTGAGGCCATGCCAGGCCAGCAAGATGCCAGTGGGCTC 240		
QY	296	CCTTCCTCTGCTGGATTCCTAGAACACACAGCTAGCCAGAACAGCTGCA 355		
Db	241	CCTTCCTCTGCTGGATTCCTAGAACACAGCTAGCCAGAACAGCTGCA 300		
QY	356	TCTCATGGCACATGCCCATGGTAGCCAGGTGAACCTGTGACA 415		
Db	301	TCTCATGGCACATGCCCATGGTAGCCAGGTGAACCTGTGACA 360		
QY	416	GTGTCCA GCGGAACCTATGCTCTGAGATGGTACCAA GCAAGCTGGCGTGTGCA 475		
Db	361	GTGTCCA GCGGAACCTATGCTCTGAGATGGTACCAA GCAAGCTGGCGTGTGCA 420		
QY	476	CAGTGCCTGGCCGACCTTAACAGGATGAGATGGCATGAAATGCCATGACTG 535		
Db	421	CAGTGCCTGGCCGACCTTAACAGGATGAGATGGCATGAAATGCCATGACTG 480		
QY		Query Match 83.2%; Score 486; DB 2; Length 526;		
		Best Local Similarity 97.7%; Pre. No. 1.e-108;		
		Matches 514; Conservative 0; Mismatches 10; Indels 2; Gaps 2;		
QY		52 CCTTCCTCTGCCCCGGCTGGATGCGCTGGAGCGAGCTGGCTCCC 111		
Db		1 CCTTCCTCTGCCCCGGCTGGATGCGCTGGAGCGAGCTGGCTCCC 60		
QY		112 GG-CGGCGCCGCTGGCTGGATGCGCTGGAGCGAGCTGGCTCCC 170		
Db		61 GCGCCGGAGAGGGCTGGATGCGCTGGAGCGAGCTGGCTCCC 120		
QY		171 CGGGCGCCCGCCGCTGGATGCGCTGGAGCGAGCTGGCTCCC 229		
Db		121 CGGGCGCCCGCCGCTGGATGCGCTGGAGCGAGCTGGCTCCC 180		
QY		230 CAGTGCCTGGCCGACCTTAACAGGATGAGATGGCATGAAATGCCATGACTG 289		

Best Local Similarity	95.1%	Pred. No.	1.e-107;
Matches	558;	Mismatches	23;
Conservative	0;	Indels	6;
Gaps	6		
Qy	1	GGCGCGGNNNGNNGCAGGTGCTAGCCCAACAGTCAGCCAAAGAGC	349
Db	220	GGCGCGGCGCGTGGCGAGTGTGAGGCCCTTGCCTTGCCTCCCTCC	60
Qy	61	TCTGCCCGGCGATCACAGTCAGCCATGGGTTGGAGGATGGCTCCGGG	119
Db	280	TCTGCCGAGCATGGGTTGGAGGATGGCTCCGGCGGGA	339
Qy	120	GGCGCGGCGGATGGGCTGGGAGAGCAGCCGATTCCAGCTGCCGCC	179
Db	340	GGCGCGGCGGATGGGCTGGGAGAGCAGCCGATTCCAGCTGCCGCC	399
Qy	180	CC-GCCACCTTGAGTCCGGTCAAGCATGGGACCTCTCCAGACGACCG	238
Db	400	CCGGCGGCCCTGGAGTCCGGGTTCAAGCATGGGACCTCTCCAGACGACCG	459
Qy	239	CCTCCCTCTGACCCGATGCCGAGTCAGCCGAGTCAATCGGGCTCCCT	298
Db	460	CCTCCCTCTGACCCGATGCCGAGTCAGCCGAGTCAATCGGGCTCCCT	519
Qy	299	TCTCTGCTGGATGCTTGGACCCAGCTAGCCAGAACGAA-GGCCCTCGAATC	357
Db	520	TCTCTGCTGGATGCTTGGACCCAGCTAGCCAGAACGAA-GGCCCTCGAATC	579
Qy	358	TCACTGGCAC-ATACGGCATGTTACCGCATGTTACCTGTGCAAG	416
Db	580	TCACTGGCAC-ATACGGCATGTTACCGCATGTTACCTGTGCAAG	639
Qy	417	TGTCGAGCAGGAACCTATGTCAGCTGAGTACCTGTGCAAG	475
Db	640	TGTCGAGCAGGAACCTATGTCAGCTGAGTACCTGTGCAAG	699
Qy	476	CAGTGGCCCTGGGACCTTACAGGCATGAGATGGATGACAAAGGCTGCGCAG	534
Db	700	CAGTGGCCCTGGGACCTTACAGGCATGAGATGGATGACAAAGGCTGCGCAG	759
Qy	535	GTAGTCAGCCATGCCATGGCAATGAGATGGAAATTACCTGGTGT	581
Db	760	GTAGTCAGCCATGCCATGGCAATGAGATGGAAATTACCTGGTGT	806
RESULT	5		
LOCUS	B1544644	875 bp	mRNA
DEFINITION	60324229.F1 NIH_MGC_95	Homo sapiens	clone IMAGE:5284679
VERSION	5		
SOURCE	mRNA sequence.		
ACCESION	B1544644		
ORGANISM	Homo sapiens (human)		
REFERENCE	1 (bases 1 to 875)		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapsb@mail.nih.gov DNA Library Preparation: Miklos Palkovits, M.D., Ph.D. DNA Library Arrayed by: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) DNA Sequencing by: Incyte Genomics, Inc.		
Tissue Procurement	Miklos Palkovits, M.D., Ph.D.		
cDNA Library Preparation	Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)		
CDNA Library Arrayed by	The I.M.A.G.E. Consortium (LILN)		
DNA Sequencing by	Incyte Genomics, Inc.		
Clone distribution	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: http://image.llnl.gov		
Plate	LILAM1719	row: h	column: 24
High quality sequence	scop: 785.		
Location/Qualifiers	1..875		
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/db_xref="taxon:9606"			
/clone="IMAGE:5284679"			
/tissue_type="hippocampus"			
/lab_host="IDH108"			
/clone_id="NIH_MGC_95"			
/note="Organ: brain; Vector: plbluescriptR (modified plbluescript KS+); Site:1: BamHI; Site:2: SalI-XbaI (97cggg); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTT-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, preparation). Library constructed by M. Brownstein (NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."			
ORIGIN	Query Match		

Query Match Similarity 71.4%; Score 417.2; DB 2; Length 1118;
 Best Local Similarity 98.7%; Pred. No. 1e-91; 3; Indels 3; Gaps 3;
 Matches 452; Conservative 0; Mismatches 0;

Qy 130 GATGGCGGCTGGCGATTCCAGTCAGGAGCAGCCGGCC 180
 Db 1 GATGGCGGCTGGCGATTCCAGTCAGGAGCAGCCGGCC 60

Qy 189 TTGGCACTTCCGGTTACGGCATGGGACCTCTCCAGCAGGCCGGCTCGCTCC 248
 Db 61 CTGGCACTTCCGGTTACGGCATGGGACCTCTCCAGCAGGCCGGCTCGCTCC 120

Qy 249 TGAGGCCATGCCCGAGCAAGCCAGATCGGGCTCCCTCTCGCTT 308
 Db 241 TGAGGCCATGCCCGAGCAAGCCAGATCGGGCTCCCTCTCGCTT 180

Qy 309 GGATTCCTTAGCACACCACAGCTAGCCAGAACAGGGCTCGAAATCTATGGCACA 368
 Db 121 TCCAGGCCATGCCCGAGCAAGCCAGATCGGGCTCCCTCTCGCTT 300

Qy 181 420 CCAGCAGGAACTPATGTTCTGACCATTAACRACAAGGCCTGGGTCTGAGGT 479
 Db 181 GGATCCCTAGCACACCACAGCTAGCCAGAACAGGGCTCGAACTGGCACA 240

Qy 369 TACCGCCATGTGACCGCCAGGTAACTCTGACAAAGTGTCAGAGGA 428
 Db 241 TACCGCCATGTGACCTGGCACTGGCTGACAAAGTGTCAGAGGA 300

Qy 429 ACCATGCTCTGACATGGATTTGACCAACAGCTGGCTGCAAGTGTGTGTG 488
 Db 301 ACCATGCTCTGACATGGATTTGACCAACAGCTGGCTGCAAGTGTGTG 360

Qy 489 GGCAACCTTACAGGATGTAATGGCATAGAG-AAATGGCATAGCTGACTGAGCAT 546
 Db 361 GGCAACCTTACAGGATGTAATGGCATAGCAATGGCATAGCAATGGCTGCC 420

RESULT 9
 N49208 452 bp mRNA linear EST 14-FEB-1996
 LOCUS YY8408.81 Soares multiple sclerosis_2NBHMSP Homo sapiens cDNA
 DEFINITION clone IMAGE:2802623', mRNA sequence.
 ACCESSION N49208
 VERSION N49208.1 GI:1190374
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE I (bases 1 to 1118)
 AUTHORS NIH-MCG http://mhc.ncbi.nlm.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Unpublished Contact: Robert Strausberg, Ph.D.
 Email: cgsabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LCM296 row: o column: 04
 High quality sequence stop: 716.
 Location/Qualifiers 1..1118
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3672107"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC_39"
 /notes="Organ: pancreas; Vector: POF7; Site1: XbaI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XbaI sites using the
 following 5' adaptor: GGACGAG (G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-CDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies)."
 FEATURES source
 ORIGIN

/organism="Homo sapiens"
 /mol_type="mRNA"

FEATURES source
 COMMENT
 CONTACT Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Possible reversed clone: poly-T not found
 Seq primer: m13-40 forward
 High quality sequence stop: 390.
 Location/Qualifiers
 1..452
 1.452
 Location/Qualifiers
 /organism="Homo sapiens"

LOCUS	BQ887029	913 bp	mRNA	EST 16-AUG-2002
DEFINITION	AGENCOURT 8752338 NIH_MGC_130 Mus musculus cDNA clone IMAGE:63333538			
VERSION	5			
ACCESSION	BQ887029			
ORGANISM	Mus musculus (house mouse)			
FEATURES				
ORIGIN	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 913)			
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
TITLE				
JOURNAL	Contact: Robert Straussberg, Ph.D.			
COMMENT	Email: cgabbs-r@mail.nih.gov			
source	Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman, Ph.D. cDNA Library Preparation: ResGen, Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov/ row: o column: 11 plate: LIAM13192			
FEATURES source	1. .913 /organism="Mus musculus" /mol_type="mRNA" /db_xref="Taxon:10090" /clone="IMAGE:63333538" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 130" /note="Organ: oecystis; Vector: pCMV-SPORT6.1; Site_1: EcoRI; Site_2: NotI; Cloned unidirectionally. Primar: Oligo dt. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library." Best Local Similarity 82.0%; Conservative 493; Matches 17; Gaps 4;			
Query Match	65.9% Score 385; DB 5; Length 913; Pred. No. 8-84; Pred. No. 8-84; 0; Mismatches 91; Indels 17; Gaps 4;			
Y	1 GCGNCGGGNNNGCAAGGTCTGAGGCCCT-AGNGCCTCCCTTCGCCCTCCCTC 59 221 GCGCCASGCCCTGGGA-GGTCTGAGGCCCTTCCTGAGGCCCTCCCTC 280			
b	60 CTC-----TCGCCGCGCTAGCTACATGGGTGTCAGGTGATGGCTC-C 110 281 TTCCGCCTGGCTGCTGCTGAGTCAGTGGCTCATGGGTGATGGCTC 340			
b	111 CGGCCGGAAAGCCGCGGNGCATGGCCCTGGCGAGAAGCAGGCCATTGGCTC 170 341 CGCCCGTGAGGGGGCTGGATGGGGCTGGCGAGAACAGCCACCATTCGGCTCC 400			
b	171 CGCG-----GCCCCGGAGGCCGGCTGGATGGGGCTGGCGAGAACAGCCACCATTCGGCTCC 223 401 GTGGGGGGAGGCCGGCTGGATGGGGCTGGCGAGAACAGCCACCATTCGGCTCC 460			
b	224 GAGCAGCGACCGCCCTCTGGATCACACCAAGCTGAGCCAGCGAT 283 461 AAGAGACTCTGAGTCCTCCCTGGATCACAGCTAACAGCTAACAGCAACA 520			
b	284 GATCGCGCGCTCTGGATCACACCAAGCTGAGCCAGCGAT 343 521 GTCGCGCGCTCTGGATCACACCAAGCTGAGCCAGCGAT 580			
b	344 GAGGGCTGGAATCTCATGGCACTACGGCCATGGTGAAGCTGGCGAGGTGT 403 581 AAAGACTCTGAGTCCTCCCTGGACCTAGCCATGAGCTGGGTGT 640			
b	404 AACCTGTGTAACAGTGTGCGAGGAAACCTATGTGTCATGGACATTGTGACAAAGGCT 463			

Qy	171	CCCGC-----cgccccggccacccgtcgagtcggatcccgggtcagccatgggacccttcc	223
Db	399	GTCGGCGGAGGGCCCCCTCGCCCTCGCTCAAGGCCATCGGCCGAGCTGGCCATGGGGC	458
Qy	224	GAGCAAGCAGCACGGCCCTCGCCCTCGCTCAAGGCCATCGGCCGAGCTGGCCATGGCGAT	283
Db	459	AACAGCACTACGGCCCTCGCTCAAGGCCATCGGCCGAGCTGGCCATGGCGAT	518
Qy	284	GATCGGGGGTCCCTCCCGCTCGTGTGGATTCTTAGCACACCACAGCTCGCCAGAACAA	343
Db	519	GTCGGCGGCTCTCCCTCCCGCTCGCTCAAGGCCATCGGCCGAGCTGGCGAT	578
Qy	344	GAAGGCTCTGAATCTCATTTGGACAATACCGCCATTGTGACCGTGCACCGCCAGGTGCT	403
Db	579	AARGACTCTGAGTCTCTGGACCTACCGCCATTGTGACCGTACCCACTGGCCAGTGCT	638
Qy	404	AACTGTGACAAGTGTCCAGCAGGAACCTATGTCCTGAGGATTGACCAACACAGCCCT	463
Db	639	AACCTGCGACAAGTGGCCAGCGGAACTGTCCTCGAGACTGTACCACTGGCCCT	698
Qy	464	GCGCGCTCTGCGAGCTGGCCCTGTGGGACCTTACAGGGATGAGAATGGCATAGAGAA	523
Db	699	GCGAGTCTGCGAGCTGGCCCTGTGGGACCTTACAGGGATGAGAATGGCATAGAGAG	758
Qy	524	ATGCCATGACTGTAGTCAGCATGGCCATGGCAATGAGAATTACCTTGTCTGC	583
Db	759	ATGCCATGACTGTAGTCAGCCATGTGTCATGGCGATGATGAGATTACCTTGTCTGC	818
Qy	584	C 584	
Db	819	C 819	
RESULT	13		
CA333708			
LOCUS	CA333708	645 bp mRNA linear EST 04-NOV-2002	
DEFINITION	NIH_18_01b12.y1	NCI CGAP Pr50 Rattus norvegicus cDNA clone	
	IMAGE:5599054 5'	mRNA sequence.	
ACCESSION	CA333708		
VERSION	CA333708.1	GI:24551806	
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
REFERENCE	1 (bases 1 to 645)	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicb/CGAP.	
AUTHORS		National Cancer Institute, Cancer Genome Anatomy Project (CGAP).	
TITLE		Tumor Gene Index	
JOURNAL		Unpublished (1997)	
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgaps:r@mail.nih.gov cDNA Library Preparation: cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov	
FEATURES		Plate: LLAM12387 row: C column: 23 Seq primer: M13RPL1 reverse primer (ABI). Location/Qualifiers 1. -645 /organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="taxon:10116" /clone="IMAGE:5599054" /sex="male" /tissue_type="dorsolateral prostate, pool of 3-, 5-, and 7-days post-castration" /dev_stage="adult, 11 week"	
source			

Db 419 AC 420 Qy 432 TATGTCCTGAGATTGACCAACACAGCCCTGGCTCTGAGCAGTGCCTGTGGGG 491
 Db 361 TATGTCCTGAGATTGACCAACACAGCCCTGGCTCTGAGCAGTGCCTGTGGGG 415
 RESULT 15 AL138519 497 bp mRNA linear EST 04-SEP-2003 Qy 492 ACCTTTACAGGCCATGAGAATGCCATAGAAATGCCATGACTGTAGTCAGC 543
 LOCUS DKFZp761B215_r1 761 (synonym: hamy2) Homo sapiens cDNA clone.
 DEFINITION DKFZp761B215_r1 mRNA sequence.

ACCESSION AL138519 Qy 416 GACCTTACAGGCCATGAGCAGTGCCTGTGGGG 465
 VERSION EST. Db
 KEYWORDS Homo sapiens (human)

SOURCE Unpublished (1999) Search completed: January 8, 2005, 03:53:42
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE Ansorge, W., Wirkner, U., Newes, W., Weil, B. and Wiemann, S. Job time : 3440 secs

AUTHORS Ansorge, W., Wirkner, U., Newes, W., Weil, B. and Wiemann, S.

TITLE EST (Ansorge, W., Wirkner, U., Newes, H.W., Weil, B. and Wiemann, S.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert.

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: S.wiemann@dkfz-heidelberg.de;

sequenced by EMBL (European Molecular Biology Laboratory Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.

No S1 sequence available.

This clone (DKFZp761B215) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES Location/Qualifiers

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 /db_xref="8606"
 /clone="DKFZp761B215"
 /tissue_type="amygdala"
 /dev_stage="adult"
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 /clone_lib="761 (synonym: hamy2)"
 /note="vector: psport1; site_1: NotI; site_2: SalI"

ORIGIN

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Matches 443; Conservatve 0;	Mismatches 20;	Indels 9;	Gaps 5;		
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Qy 74 AGCAGTGACATGGGTGTTGGAGTAGATGGGCTCCGG-CGGGAGGGCGGTGGAT 132					
Db 133 GCGGGCTGGCAGAGCAGCCGCCGATTCAGCTGGACCTCTCGAGCAGGCCCC-GGCCACCTTG 191					
Db 61 GCGGGCTGGCAGAGCAGCCGCCGATTCAGCTGGACCTCTCGAGCAGGCCCCCTGG 120					
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 23:48:58 ; Search time 3738 Seconds
(without alignments)

7388.225 Million cell updates/sec

Title: US-10-663-157-3

Perfect score: 584

Sequence: 1 gcgncgcgnngncaag.....agaattacccgttgtctgc 584

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database :

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2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_D1:*
9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	578	99.0	584	6	AR437901	
3	576.4	98.7	2271	6	BD263012	
4	571.6	97.9	1686	6	BD263011	
5	570	97.6	1686	6	BD263014	
6	550.2	94.2	588	6	AR437902	
7	544.8	93.3	2636	6	AX876881	
8	544.8	93.3	2636	6	BD156366	
9	544.8	93.3	2636	9	AK001504	
10	544.8	93.3	2638	6	AR134339	
11	544.8	93.3	2638	6	BD076495	
12	544.8	93.3	2877	6	BD235207	
13	544.8	93.3	3474	6	BD271797	
14	544.8	93.3	3474	6	AR200579	
15	544.8	93.3	3474	6	AR441939	
16	544.8	93.3	3474	6	BD124556	
17	543.2	93.0	3534	6	CQ767596	
18	543.2	93.0	3534	6	AX376350	
19	543.2	93.0	3534	9	AY358304	

AR134328 Sequence

BD076484 Novel mol

BD235206 Mammalian

BD261788 Tumor nec

BC016420 Mus muscu

BD263013 Nucleic a

BC017730 Homo sapi

E29452 Tumor necro

AR437900 sequence

BD261794 Tumor nec

AR134310 Sequence

BD076486 Novel mol

BD235208 Mammalian

AR134310 Sequence

BD076496 Novel mol

BD261789 Tumor nec

AX327471 Sequence

AX658233 Sequence

AX706993 Sequence

AF068866 Homo sapi

BR007420 Homo sapi

BT009883 Synthetic

BD261790 Tumor nec

BD263015 Nucleic a

AY043489 Mus muscu

AF322069 Mus muscu

ALIGNMENTS

RESULT 1

E29453

LOCUS

E29453

DEFINITION

Tumor necrosis-associated receptor TR7.

ACCESSION

E29453-1 GI:13025565

VERSION

JP 199018786-A/2.

SOURCE

unidentified

ORGANISM

unclassified

REFERENCE

1 (bases 1 to 584)

AUTHORS

Keith, C.D., Mark, R.H., Peter, Y. and K.B.T.

TITLE

Tumor necrosis-associated receptor TR7

PATENT

JP 199018786-A 2 26-JAN-1997

AR134328 Sequence

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BD261788 Tumor nec

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AY043489 Mus muscu

AF322069 Mus muscu

C12N15/10, PC

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AR437900 sequence

BD261794 Tumor nec

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AR134310 Sequence

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DEFINITION	Nucleic acids encoding osteoprotegerin-like proteins and methods of using same.				
ACCESSION	BD263012				
VERSION	1				
KEYWORDS	GI:33072780				
SOURCE	JP 2002528067-A/2.				
ORGANISM	Homo sapiens (human)				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 2271)				
AUTHORS	Shimkets,R.A., Yang,M., Lichenstein,H. and McDonald,W.F.				
TITLE	Nucleic acids encoding osteoprotegerin-like proteins and methods of using same				
JOURNAL	Patent: JP 2002528067-A 2 03-SEP-2002;				
COMMENT	CURAGEN CORP				
OS	Homo sapiens (human)				
PN	JP 2002528067-A/2				
PD	03-SEP-2002				
PF	22-OCT-1999	JP 20000578341			
PR	23-OCT-1998	US 60/10481, 01-OCT-1999	US	60/156993 PR	
	21-OCT-1999 US 09/422680				
PI	RICHARD A SHIMKETS,MEIJIA YANG,HENRI LICHENSTEIN,WILLIAM F MCDONALD				
PC	C12N15/09,A61K31/711,A61K38/00,A61K39/395,A61K45/00,				
PC	C12N1/19,A61P19/00,				
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source	1. .2271	Score 576.4; DB 6; Length 2271;	PR 23-OCT-1998 US 60/105481,01-OCT-1999 US 60/156993 PR 21-OCT-1999 US 09/42280 PI RICHARD A. SHIMKETS, MEIJIA YANG, HENRI LICHENSTEIN, WILLIAM F. PI
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Db	1 GCGNCGGNNNGCAAGTGTGAGGCCCTTAGNCCTCCCTGGCCCTCCCTCC 60	Db	1 TCGCCCTCAGCCATGGCGTAGCAAGTCAGGTTGGAGTAGATGGCTCCGGCGAG 120 1 TCGCCCTCAGCCATGGCGTAGCAAGTCAGGTTGGAGTAGATGGCTCCGGCGAG 120
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Qy	481 GCCCTGTGGGACCTTACAGGATGAGAATGGCATGACTGACTC 540	Qy	481 GCCCTGTGGGACCTTACAGGATGAGAATGGCATGACTGACTC 540 481 GCCCTGTGGGACCTTACAGGATGAGAATGGCATGACTGACTC 540
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Qy	541 AGCCATGGCCATGGCCAATGATTGAGAAATTACCTTGCTGCC 584	Qy	541 AGCCATGGCCATGGCCAATGATTGAGAAATTACCTTGCTGCC 584 541 AGCCATGGCCATGGCCAATGATTGAGAAATTACCTTGCTGCC 584
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RESULT 4		RESULT 5	BD263014 LOCUS BD263014 DEFINITION DEFINITION KEYWORDS Nucleic acids encoding osteoprotegerin-like proteins and methods of SOURCE Homo sapiens (human) using same. ORGANISM Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo. REFERENCE Shimkets, R.A., Yang, M., Lichenstein, H. and McDonald, W.F., Authors Nucleic acids encoding osteoprotegerin-like proteins and methods of TITLE using same. JOURNAL Patent: JP 2002528067-A 1 03-SEP-2002; COMMENT TURGEN CORP OS Homo sapiens (human) PN JP 2002528067-A/1 PD 03-SEP-2002 PF 22-OCT-1999 JP 2000578341 BD263014 VERSION GI:33072782

Qy	539	TCA GGC ATG CCA TGG CCA ATG ATT GAA ATT ACC TT GTG CTG GCC	584		DEFINITION Novel molecules of TNF receptor super family and utilization thereof.
Db	724	TCAGCCATGCCATGGCCATGGCCATGGCCATGGCCATGGCCATGGCC	769		ACCESSION BD076495
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AR134339	AR134339	Sequence 22 from patent US 6194151.	2638 bp	DNA	SOURCE JP 2001517443-A/13.
LOCUS	AR134339				ORGANISM unidentified
DEFINITION	Sequence 22 from patent US 6194151.				REFERENCE 1 (bases 1 to 2638)
ACCESSION	AR134339				AUTHORS Busfield, S.J.
VERSION	AR134339.1				TITLE Novel molecules of TNF receptor super family and utilization thereof
KEYWORDS					JOURNAL Patent: JP 2001517443-A 13 OCT-2001;
SOURCE	Unknown.				COMMENT OS Unidentified
ORGANISM	Unclassified.				PN JP 2001517443-A/13
REFERENCE	1 (bases 1 to 2638)				PD 0/OCT-2001
AUTHORS	Busfield, S.J.				PF 25-SEP-1998 JP 2000512955
TITLE	Molecules of the TNF receptor superfamily and uses therefor				PR 26-SEP-1997 US 08/938896, 17-MAR-1998 US 09/042785 PI
JOURNAL	Patent: US 6194151-A 22 FEB-2001;				SAMANTHA J BUSFIELD
FEATURES	Location/Qualifiers				PC C12N5/09, C07K16/28, C12N5/10, C12P21/02, C12Q1/68, G01N33/53, PC G01N33/53,
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					CC Topology: Linear;
					CC Novel molecules of TNF receptor super family and utilization thereof
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Qy	1	GCG NCG GGN GNG GAG GTG CTG GAG GGC C CC TAG NC C T C C C C C C C C	60		FEATURES source
Db	299	GCG GCG CGC GGT GG AGT GG CAG GT GAG GC C C C C C C C C C C C C	358		ORIGIN
Qy	61	TCT GCG CCG GCG CGTAG CAG GCG GAT GGG GTG TGG AGG TGA GAT GGG C C C G G	119		Query Match 93.3%; Score 544.8; DB 6; Length 2638;
Db	359	TCT GCG CCG GCG CGACCG TGC ACAT GGG GTG TGG AGG TGA GAT GGG C C C G G	418		Best Local Similarity 97.4%; Pred. No. 1..2e-101;
Qy	120	GCG GCG GGT GGT GAT GGG CCG GAG GAG CAG GCG C C C C C C C C C C C C	179		Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;
Db	419	GCG GCG GGT GAT GGG CCG GAG GAG CAG GCG C C C C C C C C C C C C C	478		Qy 1 GCG NCG GGN GNG GAG GTG CTG GAG GGC C CC TAG NC C T C C C C C C C C
Qy	180	CC..GCG CAC CT TGG GAG TCCC CG GGT CA GCG AT GGG GCT CTC GAG C C C C C	238		Db 299 GCG GCG GCG CCG GGT GAG GGT GCT GAG C C C C C C C C C C C C C C
Db	479	C CG GCG C C C C T G C G A T G C C C C G G T C A G C C A T G G G A C C T C C G	538		Qy 61 TCT GCG CCG GCG CGTAG CAG TGG GGT GAG GGT GAT GGG C C C C C C C C C C
Qy	239	CCT GCG CCT CTC T G C A G C G C G G C A T G C G C G G C A G C G C G G C A G C G C	298		Db 359 TCT GCG CCG GCG AGT GGG GCT GAG CAG GCG GAT TGG GGT GAG GGT GAT GGG C C C C C C C C C C C C C C
Db	539	CCT GCG CCT CTC T G C A G C G C G G C A T G C G C G G C A G C G C G G C A G C G C	598		Qy 120 GCG GCG GGT GGT GAT GGG CAG AAG CAG CCG GGT GAG GGT GAT GGG C
Qy	299	TCT C T G C T G G A T T C T G A C C A C A G C T C A G G C T C A G G C T C A G G C T	358		Db 419 GCG GCG GGT GGT GAT GGG CAG AAG CAG CCG GGT GAG GGT GAT GGG C
Db	599	TCT C T G G T G G A T T C T G A C C A C A G C T C A G G C T C A G G C T C A G G C T	658		Qy 180 CC..GCG CAC CT TGG GAG TCCC CG GAG GAG CAG GCG C C C C C C C C C C C C
Qy	359	CAT T GCG C A T A C C C C A T G T G A C C A C A G C T C A G G C T C A G G C T C A G G C T	418		Db 479 CCT GCG CCT CTC T G C A G C G C G G C A T G C G C G G C A G C G C G G C A G C G C
Db	719	TCCACGAGGAAACCTATGTCACCATGTCAGGCTGCTGCGAG	778		Qy 299 TCT GCG CCG GGT GAT C C C T A G C A C C A C A G C T C A G G C A G A G G C C T G C G A A T C T
Qy	479	TTCGCCCTGGGGACCTTACAGGCTAAGGCTAAGGCTAATGCAATGACTGTAG	538		Db 599 TCT GCG CCT CTC T G C A G C C A C C A C A G C T C A G G C A G A G G C C T G C G A A T C T
Db	779	TTCGCCCTGGGGACCTTACAGGCTAAGGCTAAGGCTAATGCAATGACTGTAG	838		Qy 359 CAT T GCG C A T A C C C C A T G T G A C C A C A G C T C A G G C T C A G G C A G A G G C C T G C G A A T C T
Qy	539	TCA GGC ATG CCA TGG CCA ATG ATT GAA ATT ACC TT GTG CTG GCC	584		Db 659 CCT GCG CAC AT C C C C C A T G C G C G G C A T G C G C G G C A G C G C G C
Db	839	TCA GGC ATG CCA TGG CCA ATG ATT GAA ATT ACC TT GTG CTG GCC	884		Qy 419 TCCAGCAGGAAACCTATGTCACCATGTCAGGCTGCTGCGAG
RESULT 11					Db 719 TCCAGCAGGAAACCTATGTCACCATGTCAGGCTGCTGCGAG
BD076495					Qy 479 TTGGCCCTGGGGACCTTACAGGCTAAGGCTAATGCAATGACTGTAG
LOCUS	BD076495				Qy

Qy	779	TTCGCCCTGTGGGACCTTTAACCGGATCAATGATTGAGAATTACCTTGCTGTAG	838	Y	120	GCGCCGGTGGATGGCTGGGAGAGCAGGGCCGATTCGGCTGGCTGGGCC	378																												
Db	539	TGAGCCATGCCCATGCCATGCCCCATGATTGAGAATTACCTTGCTGTGCC	584	Db	319	GCGGGGGTGGATGGCTGGGAGAGCAGGGCCGATTCGGCTGGCTGGGCC	378																												
Db	839	TGAGCCATGCCCATGCCATGCCCCATGATTGAGAATTACCTTGCTGTGCC	884	Y	180	CC-GSCCACCTGGAGTCCTCCGGTTCAGCCATGGGACTCTGGAGCAGGCC	238																												
RESULT 12	BD235207	BD235207	2877 bp DNA linear	PAT 17-JUL-2003	Db	379	CCTGGCCTGGATGGCTGGGATGGCTGGATGGCTGGCTGGCTGGGCC	438																											
LOCUS DEFINITION	Mammalian Genes; dendritic cell prostaglandin-like transporter (DC-PGT), HsLJD37R and RANKL, HCCS chemokine, deubiquitinases 11 and 12 (DUB11, DUB12), MD-2 and cyclin E2, and reagents and methods relating thereto.	Y	239	CCTGGCCTGGATGGCTGGGATGGCTGGATGGCTGGCTGGCTGGGCC	298																														
ACCESSION VERSION	BD235207 BD235207.1 GI:33044977	Y	299	TCTGCCTGGTGGATTCCTAGACCAACCAGCTAGCCAGGCAAGCCACG	358																														
KEYWORDS SOURCE	JP 2002519062-A/4.	Db	439	TCTGCCTGGTGGATTCCTAGACCAACCAGCTAGCCAGGCAAGCCACG	498																														
ORGANISM	unclassified	Y	499	TCTGCCTGGTGGATTCCTAGACCAACCAGCTAGCCAGGCAAGCCACG	558																														
REFERENCE AUTHORS	1 (bases 1 to 2877) Bates, E. E. M., Lebecque, S. J. E., Murphy, E. B., Mattson, J. D., Gorham, D. M., Hedrick, J. A., Wang, L. J., Zlotnik, A., Murgolo, N. J., Greene, J. R., Johnston, J. A., Bazzan, J. F., Mahony, D. and Lees, E. M.	Db	559	CATGGCACATAACGGCATGGTGAACCTGGTCAACCTGTGACAAGTG	418																														
TITLE	Mammalian genes HsLJD37R and RANKL, HCCS chemokine, deubiquitinases 11 and 12 (DUB11, DUB12), MD-2 and cyclin E2, and reagents and methods relating thereto.	Y	419	TCCAGCAGAACCTATGGCTCTGAGATGTACCAACAGGCTCTGGCAG	478																														
JOURNAL	Patent: JP 2002519062-A 4 02-JUL-2002;	Db	619	TCCAGCAGAACCTATGGCTCTGAGATGTACCAACACAGGCTCTGGCAG	678																														
COMMENT	OS Unknown	Y	479	TTGCCTGTGGGACCTTACAGGCTATGAAATGGCATAGAGAATGGCTAGTGTAG	538																														
PN	JP 2002519062-A/4	Db	679	TTGCCTGTGGGACCTTACAGGCTATGAAATGGCATAGAGAATGGCTAGTGTAG	738																														
PD	02-JUL-2002	Y	539	TCAAGCCATGCCCATGGCCAATGATTGAGAAATTACCTTGCTGCC	584																														
PF	06-JUL-1999 JP 2000058207	Db	739	TCAAGCCATGCCCATGGCCAATGATTGAGAAATTACCTTGCTGCC	784																														
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23-JUL-1998 US 60/093367-12-AUG-1998 US 09/132968 PR	LOCUS DEFINITION	Human tumor necrosis factor receptor TR9.	3474 bp DNA	linear	Human tumor necrosis factor receptor TR9.	3474 bp DNA	PAT 17-JUL-2003																												
18-AUG-1998 US 09/136134-11-SEP-1998 US 60/099999 PI	ACCESSION NUMBER	BD271797	BD271797	BD271797	BD271797	BD271797	PAT 17-JUL-2003																												
ELIZABETH ESTHER MARY BATES, SERGE J E LEBECQUE, ERIN E MURPHY, PI	KEYWORDS	GI:33081565	JP 2002542771-A1	JP 2002542771-A1	JP 2002542771-A1	JP 2002542771-A1	PAT 17-JUL-2003																												
JEANINE D MATTSON, DANIEL M GORMAN, JOSEPH A HEDRICK, LUQUAN WANG, ALBERT ZLOTNIK, NICHOLAS J MURGOLO, JONATHAN R GREENE, JAMES A JOSE FERNANDO BAZAN, DANIEL MAHONY, EMMA M LEES, PC C12N15/09, A61K38/00, A61K38/46, A61P43/00, C07K14/47, C07K16/18, PC C07K16/24,	SOURCE	Homo sapiens (human)	PAT 17-JUL-2003																																
PI	PI	PI	PI	PI	PI	PI	PAT 17-JUL-2003																												
PI	PI	PI	PI	PI	PI	PI	PAT 17-JUL-2003																												
PC	PC	PC	PC	PC	PC	PC	PAT 17-JUL-2003																												
CC	CC	CC	CC	CC	CC	CC	PAT 17-JUL-2003																												
FT	FT	FT	FT	FT	FT	FT	PAT 17-JUL-2003																												
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Qy	180	CC-GGCCAACCTTGGAGTCCCCTGGGTTCAACATGGGAACTCTCGAACAGCACGGC	238
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Qy	359	CATGGCACATAACGGCATGTTGACCGAACAGCTTGACCGAACAGGCTTGAACT	418
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Search completed: January 8, 2005, 02:56:18
 Job time : 3743 secs

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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 22:11:19 ; Search time 521 Seconds
(without alignments)

5884.188 Million cell updates/sec

Title: US-10-663-157-3

Perfect score: 584

Sequence: 1 ggcgcgcggangngcaag.....agaattacccgtgtgcc 584

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Result No.	Score	Query	Match	Length	DB ID	Description
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3	571.6	97.9	1686	3	AAA28724	Aaa28724 Human ost
4	571.0	97.6	1686	3	AAC28726	Aaa28726 Human ost
5	546.4	93.6	2646	2	AAX25260	Aax25260 Human ost
6	546.4	93.6	2686	2	AAX25261	Aax25261 Tumour ne
7	546.4	93.6	3440	2	AAX25259	Aax25259 Human ful
8	544.8	93.3	2636	4	AAH1474	Aah1474 Human CDN
9	544.8	93.3	2638	2	AAX25322	Aax25322 Human TNF
10	544.8	93.3	2877	3	AAZ2406	Aaz2406 CDNA enco
11	544.8	93.3	2877	8	AAL53945	Aal53945 2877nt 10
12	544.8	93.3	3474	2	AAV9927	Aav9927 Novel hum
13	544.8	93.3	3474	3	AAC99558	Aaa99558 Human tum
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20	543.2	93.0	3534	8	ACA73593	Aca73593 Human sec
21	543.2	93.0	3534	8	ACA05508	Aca05508 Human sec

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29	543.2	93.0	3534	8	ACAT7365	Novel hum
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32	543.2	93.0	3534	8	ACD0357	Human sec
33	543.2	93.0	3534	8	ACB88791	Novel hum
34	543.2	93.0	3534	8	ACAT0233	Human sec
35	543.2	93.0	3534	8	ACD12455	Novel hum
36	543.2	93.0	3534	8	ACC74370	Human sec
37	543.2	93.0	3534	8	ACD15998	Human sec
38	543.2	93.0	3534	8	ACD25566	Novel hum
39	543.2	93.0	3534	8	ACD18043	Human sec
40	543.2	93.0	3534	8	ACCB88330	Human sec
41	543.2	93.0	3534	8	ACD21684	Human sec
42	543.2	93.0	3534	8	ACD18751	Human sec
43	543.2	93.0	3534	8	ACA71677	Human sec
44	543.2	93.0	3534	8	ABX98361	Human CDN
45	543.2	93.0	3534	8	ACD14112	Human PRO

ALIGNMENTS

RESULT 1
AAV57442
ID AAV57442 standard; cdDNA; 584 BP.
XX AC AAV57442;
XX DT 21-DEC-1998 (first entry)
XX DB Human tumour necrosis factor related receptor TR7 cdDNA fragment.
XX KW Tumour necrosis factor related receptor; TR7; human; inflammation;
KW arthritis; septicemia; autoimmune disease; psoriasis;
KW inflammatory bowel disease; infection; graft-versus-host disease;
KW transplant rejection; stroke; acute respiratory disease syndrome;
KW ischaemia; restenosis; brain injury; AIDS; bone disease; cancer;
KW atherosclerosis; Alzheimer's disease; diagnosis; therapy; vaccine; ss.
XX OS Homo sapiens
XX PH Key
FT CDS
FT FT
FT FT
FT FT
Location/Qualifiers
XX 210..584
/*tag= a

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	578	99.0	584	2	AAV57442	Aav57442 Human tum
2	576.4	98.7	2271	3	AAA28728	Aaa28728 Human ost
3	571.6	97.9	1686	3	AAA28724	Aaa28724 Human ost
4	571.0	97.6	1686	3	AAC28726	Aaa28726 Human ost
5	546.4	93.6	2646	2	AAX25260	Aax25260 Human ost
6	546.4	93.6	2686	2	AAX25261	Aax25261 Tumour ne
7	546.4	93.6	3440	2	AAX25259	Aax25259 Human ful
8	544.8	93.3	2636	4	AAH1474	Aah1474 Human CDN
9	544.8	93.3	2638	2	AAX25322	Aax25322 Human TNF
10	544.8	93.3	2877	3	AAZ2406	Aaz2406 CDNA enco
11	544.8	93.3	2877	8	AAL53945	Aal53945 2877nt 10
12	544.8	93.3	3474	2	AAV9927	Aav9927 Novel hum
13	544.8	93.3	3474	3	AAC99558	Aaa99558 Human tum
14	544.8	93.3	3662	1	ADN9552_0	Adn9552_0 Human BEC
15	543.2	93.0	3534	2	AAZ333945	Aaz333945 Human PRO
16	543.2	93.0	3534	3	AAC78474	Aac78474 Human PRO
17	543.2	93.0	3534	4	AAS46133	Aas46133 Human DNA
18	543.2	93.0	3534	8	ACA6313	Aca6313 Novel hum
19	543.2	93.0	3534	8	ACA89583	Aca89583 CDNA enco
20	543.2	93.0	3534	8	ACA73593	Aca73593 Human sec
21	543.2	93.0	3534	8	ACA05508	Aca05508 Human sec

Disclosure; Page 21-22: 25pp; English.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

WPI; 1998-50493/44.

P-SPDB; AAW75793.

New tumour necrosis factor receptor TR7 polypeptides and polynucleotides useful as diagnostic reagents and for treating Alzheimer's disease, AIDS and cancer.

RESULTS

AAA28724 standard; DNA; 1686 BP.

AAA28724;

29-AUG-2000 (first entry)

Human osteoprotegerin-like 1 (OPGx1) DNA.

OPGx1; osteoprotegerin-like; DR6 TNF-related death receptor agonist; inhibitor; bone inhibitor; vascular calcification; apoptosis; osteopathia; chromosome 6p11.1; D6s421; 88.

omo sapiens. ey DS	Location/Qualifiers 100. .94 /*tag= a /product= "Orgx1"	CD2000024771-A2. 4 -MAY -2000. 2 -OCT -1999; 3 -OCT -1998; 11 -OCT -1999; 11 -OCT -1999;	99R0-US024913. 98US -0105481P. 99US -0155993P. 99US -00422680.
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(CURA-) CURAGEN CORP.
 Shimkets RA, Yang M, Lichenstein H, McDonald WF;
 WPI: 2000-350692/30.
 P-PSDB; AA92842.

Nucleic acids encoding osteoprotegerin-like (OPG_X) polypeptides, useful for treating disorders associated with bone metabolism, such as osteoporosis and osteotetrosis.

Claim 1: Fig 1; 81pp; English.
Osteoprotigin-like polypeptides (OPGx) are expressed in bone, lymph node, germinal B cells and kidney. There appear to be at least two splice variants of this gene, a transmembrane form and an extracellular domain form. Human OPGx1, 2 and 4 contain a 36 amino acid extension at their N-

CC	terminal relative to the DR6 tumour necrosis factor (TNF)-related death receptor.
CC	The OPGX gene has been mapped to chromosome 6p11.1, essentially on top of D6S432. The OPGx polypeptides, agonists and antibodies are useful in methods to inhibit osteoclast-mediated bone resorption or vascular calcification and to modulate cell death (apoptosis). This is useful for treating disorders associated with bone metabolism, such as osteoporosis, osteopetrosis, or a condition characterized by loss of bone, breakdown of tissue, or excessive reabsorption of bone tissue
XX	Sequence 1686 BP; 438 A; 429 C; 408 G; 406 T; 0 U; 5 Other;
SQ	Query Match 97.9%; Score 571.6; DB 3; Length 1686; Best Local Similarity 99.1%; Pred. No. 5e-124; N matches 5; Indels 0; Gaps 0;
Qy	1 GCGGCCGCGGNGNCAGTGGCTAGGCCCTCTAGNGCTCCCTTGCCCCCTCCCTCC 60 1 GCGGCCGCGGNGNCAGTGGCTAGGCCCTCTAGNGCTCCCTTGCCCCCTCCCTCC 60
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Db	181 CGGCCACCTTGAGATGCCCGGTTAGCCATGGGAACTCTCCGAGCAGCACGCC 240 181 CGGCCACCTTGAGATGCCCGGTTAGCCATGGGAACTCTCCGAGCAGCACGCC 240
Qy	241 TCGGCCCTCTGGAGCCCATCCCCGGGAGGCAACCCACATGATGCCGGCTCCCTC 300 241 TCGGCCCTCTGGAGCCCATCCCCGGGAGGCAACCCACATGATGCCGGCTCCCTC 300
Db	301 TCTGTGTTGGATTCTTAGACCAACAGCTAGGCCAACAGAGGCTCTCGAATCTCA 360 301 TCTGTGTTGGATTCTTAGACCAACAGCTAGGCCAACAGAGGCTCTCGAATCTCA 360
Qy	361 TTGGCACATACCGGCTATGTTGACCTGGCCACGGCTAACCTGTCACAGTGTC 420 361 TTGGCACATACCGGCTATGTTGACCTGGCCACGGCTAACCTGTCACAGTGTC 420
Db	421 CAGCAGGAACCTATGTCCTGAGCATTTGACCAAACAAGCTGCCGTCAGGAGTT 480 421 CAGCAGGAACCTATGTCCTGAGCATTTGACCAAACAAGCTGCCGTCAGGAGTT 480
Qy	481 GCCCTTGGGGACCTTTACCGGATGAGATGGCTAGAATCCCATGACTGTAGTC 540 481 GCCCTTGGGGACCTTTACCGGATGAGATGGCTAGAATCCCATGACTGTAGTC 540
Qy	541 AGCCATGCCCATGCGAACATGTTGAGAAATTACCTGTGCTGCC 584
Db	541 AGCCATGCCCATGCGAACATGTTGAGAAATTACCTGTGCTGCC 584

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 XX WO200024771-A2.
 PN XX 04-MAY-2000.
 PD XX 22-OCT-1999; 99WO-US024913.
 PF XX 23-OCT-1998; 98US-0105481P.
 PR XX 01-OCT-1999; 99US-0156993P.
 PR 21-OCT-1999; 99US-00422680.
 XX
 PA (CUBA-) CURAGEN CORP.
 XX Shimkets RA, Yang M, Lichenstein H, McDonald WF;
 PI XX WPI; 2000-350692/30.
 DR P-PSDB; AAY92844.
 XX
 PT Nucleic acids encoding osteoprotegerin-like (OPGx) polypeptides, useful
 PT for treating disorders associated with bone metabolism, such as
 PT osteoporosis and osteopetrosis.
 XX
 PS Claim 1; Fig 6; Bipp; English.
 XX
 CC Osteoprotegerin-like polypeptides (OPGx) are expressed in bone, lymph
 CC nodes, germinal B cells and kidney. There appear to be at least two splice
 CC variants of this gene, a transmembrane form and an extracellular domain
 CC form. Human OPGx1, 2 and 4 contain 36 amino acid extension at their N-
 CC terminal relative to the DR6 tumour necrosis factor (TNF)-related death
 CC receptor. The OPGx gene has been mapped to chromosome 6p11.1, essentially
 CC on top of D6s452. The OPGx polypeptides, agonists and antibodies are
 CC useful in methods to inhibit osteoclast-mediated bone resorption or
 CC vascular calcification and to modulate cell death (apoptosis). This is
 CC useful for treating disorders associated with bone metabolism, such as
 CC osteoporosis, osteopetrosis, or a condition characterized by loss of
 CC bone, breakdown of tissue, or excessive reabsorption of bone tissue
 XX
 SQ Sequence 1686 BP; 435 A; 428 C; 406 G; 410 T; 0 U; 7 Other;
 Query Match 97.6%; Score 570; DB 3; Length 1686;
 Best Local Similarity 99.0%; Matches 578; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 DB 1 GCGNCGGNNNGCAAGGTGCTGAGCCCTCTTCTGCGCCCTCCCTCC 60
 1 GCGNCGGNNNGCAAGGTGCTGAGCCCTCTTCTGCGCCCTCCCTCC 60
 QY 61 TCTGCCGGCGTAGAGTCACATGGGTGGTAGATGGTGGAGTAGATGGTGGAG 120
 DB 61 TCTGCCGGCGTAGAGTCACATGGGTGGTAGATGGTGGAGTAGATGGTGGAG 120
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 DB 241 TCGCCCTCTGGAGCTCCGGTCACTGGCATGGCACCTCTCC 300
 QY 301 TCCCTGGATGGCTGGATGGCTGGAGGCTCGAATCTCA 360
 DB 301 TCCCTGGATGGCTGGATGGCTGGAGGCTCGAATCTCA 360
 QY 361 TTGGCACATACGCCATGTTGACCGTGCCACCGGCAAGCTGACAAGTGT 420
 DB 361 TTGGCACATACGCCATGTTGACCGTGCCACCGGCAAGCTGACAAGTGT 420

Qy 421 CAGCAGGAACCTATGTTCTGAGCTTGTACCAACAAGCTGGCGTCTGCAGCAGTT 480
 Db 421 CAGCAGGAACCTATGTTCTGAGCTTGTACCAACAAGCTGGCGTCTGCAGCAGTT 480
 Qy 481 GGCCTGTTGGGACCTTACAGGATGAGATGGCATAGAAATGCCATGACTGAGTC 540
 Db 481 GGCCTGTTGGGACCTTACAGGATGAGATGGCATAGAAATGCCATGACTGAGTC 540
 Qy 541 AGCCATGCCATGGCCATGATGGAGAAATTACCTGTGCTGCC 584
 Db 541 AGCCATGCCATGGCCATGATGGAGAAATTACCTGTGCTGCC 584

RESULT 5
 ARX25260
 ID ARX25260 standard; cDNA; 2646 BP.
 XX
 ARX25260;
 AC XX DT 19-JUN-1999 (First entry)
 DE XX Human soluble tumour necrosis factor receptor ZTNFR-6 cDNA.
 KW XX ZTNFR-6; tumour necrosis factor receptor-6; human; cell maturation;
 KW bone cell regulation; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 PT CDS 284..973
 FT /*tag= a /product= "soluble ZTNFR-6"
 FT /note= "this region of the sequence is specifically
 FT claimed in Claim 10 (b)" 284..334
 FT sig_peptide /*tag= b
 FT mat_peptide 335..973
 FT /*tag= c
 XX
 XX WO9911790-A1.
 PN XX PR 03-SEP-1998; 98WO-US018364.
 PD 11-MAR-1999.
 XX PR 04-SEP-1997; 97US-0057608P.
 PR 04-SEP-1997; 97US-00923725.
 XX PA (ZYMO) ZYMOGENETICS INC.
 PA XX PI Parrah TM, Gross JA, Matthews SM;
 DR WP1; 1999-205190/17.
 DR P-PSDB; AAV05679.
 XX
 XX New secreted or membrane bound tumor necrosis factor receptor ZTNFR-6 -
 PT useful for detecting a genetic abnormality in a patient.
 XX
 PS Claim 11a; Page 115-117; 145pp; English.
 XX
 CC This is the DNA sequence of an isolated polynucleotide that codes for a
 CC novel human soluble tumour necrosis factor receptor, designated ZTNFR-6
 CC (see AAY05679). The polynucleotide was initially identified by querying
 CC an EST database for sequences homologous to conserved motifs within the
 CC TNFR family. A second clone (see AAX25279) encodes a membrane-bound ZTNFR
 CC -6 (see AAY05678); it includes a 40 bp exon (see AAX25272) that puts the
 CC sequence in frame for the transmembrane and cytoplasmic domains of
 CC membrane-bound ZTNFR-6. The human ZTNFR-6 gene was localised to 6p21.1.
 CC The isolated polynucleotides can be utilised in the recombinant
 CC production of ZTNFR-6 polypeptides, and also in a claimed method for
 CC detecting a genetic abnormality in a patient. ZTNFR-6 polypeptides are
 CC useful in methods that promote cellular maturation and bone cell

6

X	AAX25259;	Qy	120	GGGGCCGTGGATGGAGAGCAGGGCTGGAGAAGCAGGGGATTCAGTGCCCCGGGCC
C		Db	121	GGGGCCGTGGATGGAGAGCAGGGCTGGAGAAGCAGGGGATTCAGTGCCCCGGGCC
C	19-JUL-1999	(First entry)	180	CC-GGCCACCTTGGAGCTCCCGTTAGGCCATGGGACCTCTCCGAGCAGCACCCG
T	Human full-length tumour necrosis factor receptor ZTNFR-6 cDNA.	Qy	181	cceGGGCCCTGGAGCTGGGAGGCTGGCTGAGCCCTCCGCTGGCTGGCC
X	ZTNFR-6; tumour necrosis factor receptor-6; human; cell maturation; bone cell regulation; 88.	Db	181	cceGGGCCCTGGAGCTGGGAGGCTGGCTGAGCCCTCCGCTGGCTGGCC
X	Homo sapiens.	Qy	239	CCTCGCCCTCTGCAGGGCATGCCGAGCCACAGCCACCATGATGGGGCTTCCT
S		Db	241	CCTCGCCCTCTGCAGGGCATGCCGAGCCACAGCCACCATGATGGGGCTTCCT
X	Key Location/Qualifiers	Qy	299	TCTCCCTGTTGGATTCTCTGAGCAAGCTGAACTCTGGAACTCTGGAACTCT
misc_feature	/tag= a /product= "membrane-bound ZTNFR-6"	Db	301	TCTCCCTGTTGGATTCTCTGAGCAAGCTGAACTCTGGAACTCTGGAACTCT
X	/note= "this region of the sequence is specifically claimed in Claim 10 (a)"	Qy	359	CATTGGCACATACCGGATATGGTGACCTGCCCCATGGCCACGGCAGGCTG
T	CDS	Qy	361	CATTGGCACATACCGGATATGGTGACCTGCCCCATGGCCACGGCAGGCTG
T	/tag= a	Db	419	TCCAGCAGGAACCTTAATGCTCTGAGCATTTGACCAACCAAGCTGGCGTCAGCAG
T	/product= "membrane-bound ZTNFR-6"	Qy	421	TCCAGCAGGAACCTTAATGCTCTGAGCATTTGACCAACCAAGCTGGCGTCAGCAG
T	284. .2225	Db	421	TCCAGCAGGAACCTTAATGCTCTGAGCATTTGACCAACCAAGCTGGCGTCAGCAG
T	b	Qy	479	TTCGCCCTGTGGGACCTTACCAAGCATGAGATGGCATAGAAATGCCATGACTGTAG
T	/note= "this region of the sequence is specifically claimed in Claim 10 (a)"	Db	481	TTCGCCCTGTGGGACCTTACCAAGCATGAGATGGCATAGAAATGCCATGACTGTAG
T	284. .2179	Qy	539	TGAGCATGCCATGGCAATGTTGAGAAATTACCTGTGTGTGCGC
T		Db	541	TGAGCATGCCATGGCAATGTTGAGAAATTACCTGTGTGTGCGC
T	WO9911790-A1.	Qy	586	TGAGCATGCCATGGCAATGTTGAGAAATTACCTGTGTGTGCGC
X	11-MAR-1999.			
X	03-SEP-1998;	Qy		
X	04-SEP-1997;	Qy		
R	04-SEP-1997;	Db		
R	98WU-US019364.	Qy		
X	97US-0057608P.	Db		
X	97US-00923725.	Db		
A	(ZYMO) ZYMOGENETICS INC.	RESULT 8		
I	Farrish TM, Gross JA, Matthews SM;	AHH14374	ID	AHH14374 standard; cdNA; 2636 BP.
I	WPI; 1999-205190/17.	XX	XX	
R	P-PSDB; AAY05678.	AC	AC	
R		XX	XX	26-JUN-2001 (first entry)
T	New secreted or membrane bound tumor necrosis factor receptor ZTNFR-6 - useful for detecting a genetic abnormality in a patient.	DT	DT	Human cdNA sequence SEQ ID NO:11786.
T	Claim 10a; Page 108-113; 145pp; English.	DE	DE	
X	This is the DNA sequence of an isolated polynucleotide that codes for a novel human full-length membrane-bound tumour necrosis factor receptor, designated ZTNFR-6 (see AAY05678). The polynucleotide was initially identified by querying an EST database for sequences homologous to conserved motifs within the TNFR family. A second clone (see AAX23260) encodes truncated, soluble ZTNFR-6 (see AAY05679). The full-length clone includes a 40 bp exon (see AAX25262) that puts the sequence in frame for the transmembrane and cytoplasmic domains of membrane-bound ZTNFR-6. The human ZTNFR-6 gene was localised to 6p21.1. The isolated polynucleotides can be utilised in the recombinant production of ZTNFR-6 polypeptides, and also in a claimed method for detecting a genetic abnormality in a patient. ZTNFR-6 Polypeptides are useful in methods that promote cellular maturation and bone cell regulation.	XX	XX	
X	Sequence 3440 BP;	XX	XX	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss. Homo sapiens.
X	Query Match 93.6%; Best Local Similarity 97.6%; Matches 572; Conservative	XX	XX	OS Homo sapiens.
Q	93.6%; Score 546.4; DB 2; Length 3440; 0 Other;	PN	PN	BP1074617-A2.
Y	Best Local Similarity 97.6%; Pred. No. 4..4e-118; 0: Mismatches 12; Indels 2; Gaps 2;	PR	PR	07-FEB-2001.
jb	Matches 572; Conservative	XX	XX	28-JUL-2000; 20000EP-00116126.
Y	1 GCGNCCTGGCCCTAGCAGTGCATGGGGTGTGGAGTAGTGGCTCCCTCCCTC 60	PR	PR	29-JUL-1999; 95JJP-00248036.
jb	1 GCGGCCCTAGCCTGGTGGAGGCTGAGCCCTCCCTGCGCTCCCTC 60	PR	PR	27-AUG-1999; 95JJP-00300253.
Y	61 TCTGCCCTGGCCCTAGCAGTGCATGGGGTGTGGAGTAGTGGCTCCCTCCCTC 60	PR	PR	11-JAN-2000; 20000JP-00118767.
jb	61 TCTGCCCTGGCCCTAGCAGTGCATGGGGTGTGGAGTAGTGGCTCCCTCCCTC 120	PR	PR	02-MAY-2000; 20000JP-0018767.
Y	61 TCTGCCCTGGCCCTAGCAGTGCATGGGGTGTGGAGTAGTGGCTCCCTCCCTC 120	PR	PR	09-JUN-2000; 20000JP-00241899.
X	Sequence Listing	XX	XX	XX (HELI-) HELIX RES INST.
X	Primer sets for synthesizing polynucleotides, particularly the 5'602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.	PA	PA	PA (HELI-) HELIX RES INST.
PS	Claim 8; SEQ ID NO 11786; 2537PP + Sequence Listing; English.	XX	XX	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J; Iishi S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T; WPI; 2001-318749/34.

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence [3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polymucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH0316 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence 2636 BP; 569 A; 762 C; 722 G; 583 T; 0 U; 0 Other;
 Every Match 93.3%; Score 544.8; DB 4; Length 2636;
 Local Similarity 97.4%; Pred. No. 1e-117;
 Matches 571; Conservative 0; Mi Marches 13; Indels 9 2; Gaps 2;

1 GCGNCGGGNNGNGCAAGGTGCTGGGCCCTAAGNCCTCCCTAGCCGCTCCCTCC
 60
 184 GCGGCCGGCTGGCAGGTGCTGGGCCCTAAGGCCCTCCCTAGCCGCTCCCTCC
 243
 61 TCTGCCCCCCTATGAGTGCACATGGGGTGAGGTAGATGGGCTTCGGG-CGGGAA 119

244	TCTGGCCGCCAGGTGCAATGGGTGTTGGAGTGGCTTCGGGGAA	303
120	GCGGGCGTGGATGGCGCTGGCACAGAACCGGGATTCCAGCTTCCC	179
304	GCGGGCGTGGATGGCGCTGGCACAGAACCCGGATTCCAGCTTCCC	363

1-80	CC-GGCCACCTTGCAGACTCCCCGGTTCAAGCATGGGACCTCTCGAGGAGCACCCG	238
3-64	CGGGGCCCCCTGGCAGACTCCCCGGTTCAAGCATGGGACCTCTCGAGGAGCACCCG	423
239	CCTCGGTCTTCAGGGCATGCCGGAGCAAGCAGATGCGGGCTCCCT	298

4.24	CCTCGCTTCCCTGAGCCGATGCCGGAGCAACCCACAGATGAGCGGGCTTCCT	483
2.99	TCTCCCTGCTTGATTCCTTAGCACCACAGCTAGCCAGAACAGAAGCCCTGAAATCT	358
4.84	TCTCCCTGCTTGATTCCTTAGCACCACAGCTAGCCAGAACAGAAGCCCTGAAATCT	543

604	TCCAGCAGGAACTTATCTCTAGATTGTACCAAGCAGCTGGCGTCTCAGGAG	663
479	TTGCCCTGTGGGACCTTACAGGATGGAATGGCATAGAATAAGCCATGACTGTAG	538
664	TTGCCCTGTGGGACCTTACAGGATGGAATGGCATAGAATAAGCCATGACTGTAG	723

AAX25322 standard; cDNA; 2638 BP.

19-JUL-1999 (first entry)
Human TNF receptor TRL II cDNA.
TRL II: TNF receptor-like: tumour necrosis factor receptor: human:

Homo sapiens.	
Key	Location/Qualifiers
CDS	510..2327 /*tag= a
sig_peptide	510..632 /*tag= b
mat_peptide	633..2324

WO9915663-A1.

01-APR-1999.
25-SEP-1998; 9BHQ-US020219.
26-SEP-1997; 97US-00938896.
17-MAR-1998; 98US-00012785.

Busfield SJ; WPI; 1999-254712/21.
P-PSDB; AAY05697.

Nucleic acid encoding tumor necrosis factor receptor-like protein.

This cDNA sequence codes for a novel member of the human tumour necrosis factor receptor superfamily (see MAY 05697), termed TRL II (TNF receptor-like molecule II). It contains a transmembrane domain and a cytoplasmic domain with a putative intracellular signalling motif.

human TRL II (Clone eph75L) is deposited as ATCC 98479. TRL II has a mol. wt. of 66.2 kDa. It is a membrane-bound protein that has 4 cysteine-rich domains and a C-terminal death domain (see AAY105698). TRL II cDNA was isolated from a HeLa cDNA library using mouse TRL cDNA (see AAX253201) as probe. An alternatively spliced, secreted form, human TRL I (see AAY25321), has also been identified. Chromosomal mapping located the TRL gene on chromosome 1 pp1. The invention provides full-length TRL proteins, TRL fusion proteins, antigenic peptides and anti-TRL antibodies.

host cells and non-human transgenic animals. TRL are regulators or modulators of cellular signal transduction, cellular proliferation or differentiation, cell survival and apoptosis, immune system cells, and differentiation.

be used to isolate cognate ligands, to modulate ligand/TRL interactions, to screen for potential modulators, and to treat conditions associated with abnormal TRL levels. TRL nucleic acids are used for recombinant production of TRL, to detect mutations, to identify TRL homologues, as

antisense, triplex-forming or ribozyme therapeutics, for Chromosomes mapping and for forensic identification of individuals. Antibodies, antisense sequences, TRL protein mutants etc. that modulate activity of TRL are used to treat or prevent conditions associated with aberrant TRL protein or expression e.g. cell proliferation and differentiation disorders (particularly cancer, especially of the prostate), inflammatory (e.g. arthritis) and metabolic disease (e.g. diabetes and insulin resistance).

Sequence 2638 BP; 625 A; 749 C; 701 G; 563 T; 0 U; 0 Other;

Page 8

Best Local Similarity	Pred.	No. 1e-117;	Mismatches	Indels	Gaps	2;
Matches	571;	Conservative	0;			2;
Y	1	GCGNCCCGNNNGCAAGGTGTGAGGCCCTTA				
b	299	GCGGCCGCCCCGTGGAGGTGTGAGGCCCTTA				
y	61	TCTGCCCGCCGCTGAGCAGTCATGGGTGTTGAGGTAGATGGCTCCCG-CGGGA	119			
b	359	TCTGCCGGCCGAGGTGACATGGGTGTTGAGGTAGATGGCTCCGGGGAA	418			
y	120	GCGGCCGCTGGATGGGGCTGGGGCTGGAGCAGGCCGATTCCAGCTGACCCGGCGCC	179			
b	419	GCGGCCGCTGGATGGGGCTGGGGCTGGAGCAGGCCGATTCCAGCTGACCCGGCGCC	478			
y	180	CC-GGCCACCTTGCAGTGGCCCTGGTACCCATGGGACCTCTCGAGCAGCACCGC	238			
b	479	CCGGGCCCCCTGGAGTGGCCCTGGTACCCATGGGACCTCTCGAGCAGCACCGC	538			
y	239	CCTGCCTCTGGAGCCTGGGAGGCAAGCCAGTGGATCTGGGGCTCCCT	298			
b	539	CCTGCCTCTGGAGCCTGGGAGGCAAGCCAGTGGGGCTCCCT	598			
y	299	TCTCCCTGGATTCTTAGACCACCAAGCTCAAGGAGAACAGAAGGGCTCGAAATCT	358			
b	599	TCTCCCTGGATTCTTAGACCACCAAGCTCAAGGAGAACAGAAGGGCTCGAAATCT	658			
y	359	CATTGGCACATACCGCATGGTACCGTGTGCCACGGCCGGTGTAACTCTGACAGTG	418			
b	659	CATTGGCACATACCGCATGGTACCGTGTGCCACGGCCGGTGTAACTCTGACAGTG	718			
y	419	TCCAGCAGGAACCTATGTTCTGAGCATGTCACAGCTGCGCTCTGACAGCAG	478			
b	719	TCCAGCAGGAACCTATGTTCTGAGCATGTCACAGCTGCGCTCTGACAGCAG	778			
y	479	TTGCCCTGGGACCTTACAGGCAATGAGAACATGAGAACATGACTGTAG	538			
b	779	TTGCCCTGGGACCTTACAGGCAATGAGAACATGAGAACATGACTGTAG	838			
y	539	TCAAGCCATGCCCATGCCAATGAGAACATGAGAACATGACTGTAG	584			
b	839	TCAAGCCATGCCCATGCCAATGAGAACATGACTGTAG	884			

N WO200001817-A2.
X 13-JAN-2000.
D X 06 -JUL-1999 ;
F X 06 -JUL-1998 ;
X 99WO-US012366 .
X 98US-00110938 .

Qy	299	TCTCTGCTTGGATTCCTTAGCACACCAAGCTGCCAGAACAGAAGGCCCTCGAATCT	358
Db	499	TCTCTGCTTGGATTCCTTAGCACACCAAGCTGCCAGAACAGAAGGCCCTCGAATCT	558
Qy	359	CATTGGCACATACCGCCATGTTGACCGGGCAGCTTGCTAACCTCTGACAAGTG	418
Db	559	CATTGGCACATACCGCCATGTTGACCGGGCAGCTTGCTAACCTCTGACAAGTG	618
Qy	419	TCCAGGGAAACCTATGTCTGGAATTGTACCAACACAGGCTGGCGTCTGCAGCAG	478
Db	619	TCCAGGGAAACCTATGTCTGGAATTGTACCAACACAGGCTGGCGTCTGCAGCAG	678
Qy	479	TTGCCCTGGGGACCTTACGGCATGAAATGGCATAGAAATGCTGATGCTGTAG	538
Db	679	TTGCCCTGGGGACCTTACGGCATGAAATGGCATAGAAATGCTGATGCTGTAG	738
Qy	539	TCAGGCCATGCCCAATGCCAATGATGAAATTACCCCTGGCTGCC	584
Db	739	TCAGGCCATGCCCAATGCCAATGATGAAATTACCCCTGGCTGCC	784

RESULT 11
AU53945
AU53945 standard; DNA; 2877 BP.
AU53945;
18-FEB-2003 (first entry)
2877nt long primate DNA sequence.
Cytostatic; dermatological; antiinflammatory; immunosuppressive;
antigenic; forensic analysis; abnormal physiology; autoimmune disorder;
development; abnormal proliferation; cancerous; degenerative;
systemic lupus erythematosus; inflammation; chromosomal mapping;
drug screening; gene therapy; gene; ds.

es.	Location/Qualifiers
410. .2377	
/*tag= b	
/product= "655 long primate protein"	
410. .532	
/*tag= a	
533. .2374	
/*tag= c	

Db	439	CCTCCGCTCCTCGCAGCGCATGCCAGGGCCAGGCCACAGCCAGATGATCGGGGGCTCCCT	498
Qy	299	TCTCTGCTGGATTCCTTGTGACCAACCAAGCTGCGAACAAAGGCCCTGGAATCT	358
Db	499	TCTCTGCTGGATTCCTTGTGACCAACCAAGCTGCGAACAAAGGCCCTGGAATCT	558
Qy	359	CATTGGCACATACCCCCTATGTTGACCGTGCACCCGCCAGGTGTAACCTGTCAGAAGTG	418
Db	559	CATTGGCACATACCCCCTATGTTGACCGTGCACCCGCCAGGTGTAACCTGTCAGAAGTG	618
Qy	419	TCCAGGAGGAACTATGTCTCTGACCAATGTTGACCAACACAAGCTGCGCTGTCAGCAG	478
Db	619	TCCAGGAGGAACTATGTCTCTGACCAATGTTGACCAACACAAGCTGCGCTGTCAGCAG	678
Qy	479	TTGCCCTGTTGGGACCTTACCGGATGAAATGCCATAGAAATGCCATGACCTGAGCTGAG	538
Db	679	TTGCCCTGTTGGGACCTTACCGGATGAAATGCCATAGAAATGCCATGACCTGAGCTGAG	738
Qy	539	TCAGGATGCCATGCCAAATGATTGAGAAATTACCTTGTGCTGCC	584

New isolated or recombinant polynucleotide encoding an antigenic polypeptide, e.g. HDM84, HSLD37R or RANKL, solventide, useful for

RESULT 12

ID	AAV99927 standard; DNA; 3474 BP.	Matches	571; Conservative	0; Mismatches	13; Indels	2; Gaps	2;
XX		Qy	1	GGNNCCGGNNNGCAAGGTTGCTGAGGCCCTTACAGNCCTCCCTTGCCGCCTCC 60			
AC		Db	36	GGCGCCGGCCCTGGCAGGTGCTAGGCCTCATGGGTGAGTAGGGTGGGG 95			
DT	10-MAY-1999 (first entry)	Qy	61	TCTGCCGGCGTAGCGTGCATGGGTGGTAGATGGGTGGGG 119			
XX	Novel human tumor necrosis factor receptor TR9.	Db	96	TCTGCCGGCGCAAGTGTGACATGGGTGGGGTAGATGGGTGGGG 155			
KW	Human; tumour necrosis factor receptor; TNFR; TR9 receptor; cancer; apoptosis; agonist; inhibition; autoimmune disorder; viral infection; inflammation; antagonist; AIDS; neurodegenerative disorder; ss.	Qy	120	GGGGCGGTGGTGGTGGGGTGGAGGGCTGGAGGGCTGGAGGG 179			
KW		Db	156	GGGGCGGTGGTGGTGGGGTGGAGGGCTGGAGGGCTGGAGGG 215			
XX	Homo sapiens.	Qy	180	CC-GGCCACCTTGGAGTCGGAGTCCGGATGGGACCTTCGGAGCACCGC 238			
PH	Key	Db	216	CCGGCGCCCTGGAGGGACCTTCGGAGCACGACGCCGC 275			
PT	CDS	Qy	239	CCTGCCCTCCCTCGAGGCCATGCCAGCATGGATCGGGCTGCCT 298			
PT	/*tag= a	Db	276	CCTGCCCTCCCTCGAGGCCATGCCAGCATGGATCGGGCTGCCT 335			
PT	/product= "human TR9 receptor"	Qy	299	TCTCTGTTGGATCTGGACACAGGCTCTGAATCT 358			
PT	sig_peptide	Db	336	TCTCTGTTGGATCTGGACACAGGCTCTGAATCT 395			
PT	247 . 366	Qy	359	CATTGGCACATACGCCATGGTGAACGGCAGGGTGTAACTGTGACAGTG 418			
PT	mat_peptide	Db	396	CATTGGCACATACGCCATGGTGAACGGCAGGGTGTAACTGTGACAGTG 455			
XX	W09856892-A1.	Qy	419	TCCAGCGGAAACTATGCTCTGAGCTTGTACCAACACAAGCTGGGCTGAGCAG 478			
PN		Db	456	TCCAGCGGAACTATGCTCTGAGCTTGTACCAACACAAGCTGGGCTGAGCAG 515			
XX	17-DEC-1998.	Qy	479	TTGCCCTGGGGACCTTACAGCATGGATGAGATGGATAGAAATGCCATGACTGAG 538			
PF	10-JUN-1998;	XX	516	TTGCCCTGGGGACCTTACAGCATGGATGAGATGGATAGAAATGCCATGACTGAG 575			
PF	98WO-US011932.	Qy	539	TCAGCCATGCCATGGCCAATGATGGAAATTAACCTGTGCTGCC 584			
XX	11-JUN-1997;	DB	576	TCAGCCATGCCATGGCCAATGATGGAAATTAACCTGTGCTGCC 621			
PR	97US-0052991P.						
PA	(HUMA-) HUMAN GENOME SCI INC.						
XX	PJ Ni J, Yu G, Pan P, Gentz RL;						
XX	WPI: 1999-060325/05.						
DR	P-PSDB; AAW81059.						
XX	New isolated tumour necrosis factor-like receptor, TR9 - used to develop products for treating e.g. cancers, autoimmune disorders, viral infections, inflammation, graft rejection, neurodegenerative disorders or ischaemic injury.						
XX	Claim 2: Fig 1; 134pp; English.						
PS	This is the nucleotide sequence of the human tumour necrosis factor receptor (TNFR), TR9 receptor, used in the method of the invention to develop products to treat disorders such as cancers. The novel TNFR, can be used to identify agents for modifying apoptosis. Agonists can be used to treat diseases associated with increased cell survival, or the inhibition of apoptosis, including cancers (e.g. follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumours, such as breast cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer), autoimmune disorders (e.g. systemic lupus erythematosus and immune-related glomerulonephritis rheumatoid arthritis), viral infections (e.g. herpes viruses, pox viruses and adenoviruses), inflammation, graft vs host disease, acute graft refection and chronic graft rejection. Antagonists can be used to treat diseases associated with increased apoptosis, including AIDS, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, cerebellar degeneration), myelodysplastic syndromes (e.g. aplastic anaemia), ischaemic injury (e.g. that caused by myocardial infarction, stroke and reperfusion injury), toxin-induced liver disease (e.g. that caused by alcohol), septic shock, cachexia, anorexia, inflammatory diseases and response related diseases, such as inflammatory bowel disease, rheumatoid arthritis, osteoarthritis, psoriasis and septicemia. The products can also be used for detection and diagnosis.						
XX	Sequence 3474 BP; 832 A; 895 C; 844 G; 903 T; 0 U; 0 Other;						
SQ	Query Match Score 544.8; DB 2; Length 3474; Pred. No. 1e-117.						
XX	Best Local Similarity 97.4%; Pred. No. 1e-117.						
OS	Homo sapiens.						
XX							
FT	Key						
FT	CDS						
FT	sig_peptide						
FT	mat_peptide						
	Location/Qualifiers						
	*/tag= a						
	/product= "TR9 receptor"						
	247 . 2214						
	247 . 366						
	/*tag= b						
	367 . 2214						

PR 15-MAY-1998; 98US-0085697P.
 PR 15-MAY-1998; 98US-0085704P.
 PR 15-MAY-1998; 98US-0085704P.
 PR 18-MAY-1998; 98US-0086023P.
 PR 22-MAY-1998; 98US-0086392P.
 PR 22-MAY-1998; 98US-0086414P.
 PR 22-MAY-1998; 98US-0086430P.
 PR 22-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-0087098P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 28-MAY-1998; 98US-0087208P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 11-SEP-1998; 98US-01060038P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX
 WPI; 1999-551358/46.
 DR P-PSDB; AAY41693.
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders.
 XX
 PS Claim 2; Fig 25; 530pp; English.
 XX
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as sources
 CC of probes, primers, for chromosome mapping, and for generation of
 CC antisense sequences. They can also be used to create transgenic animals.
 CC The proteins can be used to treat a variety of diseases and disorders,
 CC depending on their function. Diseases that may be treated include blood
 CC coagulation disorders, cancers and cellular adhesion disorders. They may
 CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41695 to
 CC AAY4174 represent polynucleotide and polypeptide sequence given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 3534 BP; 829 A; 927 C; 858 G; 920 T; 0 U; 0 Other;

Query Match 93.0%; Score 543.2; DB 2; Length 3534;
 Best Local Similarity 97.3%; Pred. No. 2.5e-117;
 Matches 570; Conservative 0; Mismatches -14; Indels 2; Gaps 2;

QY 1 GCGNCGGNNNGNGCAAGGTGCTGAGGCCCTATAGNCCTCCCTTGCCTCCCTCC 60
 Db 114 GCGGCGCTGGCGCTGGCAGGTGCTGAGGCCCTAGACCCCTCCCTGCCTCC 173
 QY 61 TCTGCGCCGGCGCTGGCAGGTGCTGAGGCCCTAGACCCCTCCCTGCCTCC 119
 Db 174 TCTGCGCCGGCGCTGGCAGGTGCTGAGGCCCTAGACCCCTCCCTGCCTCC 233
 QY 120 GCGCGCGTGGATGCCGCTGGCAGAAGCAGCGCGATTCCAGTAGATGGCTCCCGG-CGGGAA 179
 Db 233 GCGCGCGTGGATGCCGCTGGCAGAAGCAGCGCGATTCCAGTAGATGGCTCCCGG 293
 QY 180 CC-GGCCACCTTGCAGTCGGCTTCAAGCATGGGACTTCGGAGCACCCC 238
 Db 294 CGCGCGCCCTGGAGCTGGCTGGCTGGAGCTGGGACTTCGGAGCACCCC 353
 QY 239 CCTCGCTCTGGAGCTGGCTGGAGCTGGGACTTCGGAGCACCCC 298
 Db 354 CCTCGCTCTGGAGCTGGGACTTCGGAGCACCCC 413
 QY 299 TCTCCCTGGATGGATCCCTAGCAGAACAGCTGGCTGGAGCACCCC 358
 Db 414 TCTCCCTGGATGGATCCCTAGCAGAACAGCTGGCTGGAGCACCCC 473
 QY 359 CATTGGCACATACCGCCATGGTGGACGGCAGCTGGCTAACCTGTGACAAGTG 418
 Db 474 CATTGGCACATACCGCCATGGTGGACGGCAGCTGGCTAACCTGTGACAAGTG 533
 QY 419 TCCAGCAGGAACCTATGTCTGACCATGTAACACAGCTGGCTCGAGCAG 478

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OM nucleic - nucleic search, using sw model

Run on: January 8, 2005, 01:29:06 ; Search time 117 Seconds
(without alignments)

3547.869 Million cell updates/sec

Title: US-10-663-157-3

Perfect score: 584

Sequence: 1 gcgncgcgnngnngcaag.....agaattacccgtgtgcc 584

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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2: /cn2_6_ptodata/1/ina/5B_COMB.seq;*

3: /cn2_6_ptodata/1/ina/6A_COMB.seq;*

4: /cn2_6_ptodata/1/ina/6B_COMB.seq;*

5: /cn2_6_ptodata/1/ina/FCUS_COMB.seq;*

6: /cn2_6_ptodata/1/ina/backFiles.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	99.0	584	3 US-08-959-382-3	Sequence 3, Appli
2	578	99.0	584	4 US-09-314-844F-3	Sequence 3, Appli
3	550.2	94.2	588	4 US-09-314-844F-5	Sequence 5, Appli
4	544.8	93.3	2638	3 US-09-042-785A-22	Sequence 22, Appli
5	544.8	93.3	3474	3 US-09-527-236A-1	Sequence 1, Appli
6	529.4	90.7	2612	4 US-09-756-854-1	Sequence 1, Appli
7	381	65.2	2186	3 US-09-042-785A-3	Sequence 3, Appli
8	381	65.2	2186	4 US-09-959-382-1	Sequence 1, Appli
9	375	64.2	759	3 US-09-314-844F-1	Sequence 6, Appli
10	375	64.2	759	5 US-09-042-785A-6	Sequence 6, Appli
11	263.6	45.1	3474	4 US-09-756-854-1	Sequence 1, Appli
12	263.6	45.1	345	3 US-09-527-236A-8	Sequence 8, Appli
13	230.8	39.5	3331	3 US-09-042-785A-1	Sequence 1, Appli
14	163.2	27.9	359	4 US-09-016-434-652	Sequence 652, Appli
15	110	18.8	1719	3 US-09-042-785A-5	Sequence 5, Appli
16	44.8	7.7	12001	1 US-08-458-568A-11	Sequence 24, Appli
17	44.2	7.6	364	4 US-09-621-976-17202	Sequence 17202, A
18	41.4	7.1	152331	3 US-09-128-155-16	Sequence 16, Appli
19	41	7.0	630	4 US-09-795-226-36	Sequence 36, Appli
20	41	7.0	723	4 US-09-795-926-32	Sequence 32, Appli
21	41	7.0	965	4 US-09-795-926-34	Sequence 34, Appli
22	41	7.0	1101	4 US-09-795-926-38	Sequence 38, Appli
23	41	7.0	1812	4 US-09-795-926-42	Sequence 42, Appli
24	41	7.0	1899	4 US-09-795-926-40	Sequence 40, Appli
25	41	7.0	2712	3 US-09-025-691-4	Sequence 4, Appli
26	41	7.0	3896	4 US-09-795-926-44	Sequence 44, Appli

ALIGNMENTS

RESULT 1
US-08-959-382-3
; Sequence 3, Application US/08959382
; Patent No. 6013476
; GENERAL INFORMATION:
; APPLICANT: DEN, KEITH
; APPLICANT: HURLE, MARK
; APPLICANT: YOUNG, PETER
; APPLICANT: TAN, K.B.
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASESEQ For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,382
; FILING DATE: 28-OCT-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,796
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 584 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-959-382-3
Query Match Score 578;
Best Local Similarity 100.0%;
Pred. No. 1.8e-135;

Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Query Match Similarity 99.0%; Score 578; DB 4; Length 584; Best Local Similarity 100.0%; Pred. No. 1.8e-135; Mismatches 584; Conservative 0; Indels 0; Gaps 0;

Qy 1 GCGNCCGCGNNNGCAGGGCTGCTGAGCCCCCTAGNCCTTCCCCTCCCTCC 60
Db 1 GCGNCCGCGNNNGCAGGGCTGCTGAGCCCCCTAGNCCTTCCCCTCCCTCC 60
Qy 61 TCGGCCGCGTAGGTGCAATGGGTGGAGGTAGATGGCTCCGGAG 120
Db 61 TCGGCCGCGTAGGTGCAATGGGTGGAGGTAGATGGCTCCGGAG 120
Qy 121 GCGCGGGCTGATGGCCCTGGCGAACAGCCGCGATTCCAGTCCTCCGC 180
Db 121 GCGCGGGCTGATGGCCCTGGCGAACAGCCGCGATTCCAGTCCTCCGC 180
Qy 181 CGGCACCTTGCGAGTCGGGCTCAGGCAATGGGACCTCTGGAGBGA 240
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Db 241 TCGGCTCTGAGCGCATGGCCAGGCAAGCACAGTATCCGGGTCCCTC 300
Qy 301 TCGCGCTTGATGGATTCTTACCAACCAAGCTAGCCGAAACAGA 360
Db 301 TCGCGCTTGATGGATTCTTACCAACCAAGCTAGCCGAAACAGA 360
Qy 361 TTGGCACATACGGCCATGGTACCCGGCCAGCTGGCTAACCTGTGACAAGTGT 420
Db 361 TTGGCACATACGGCCATGGTACCCGGCCAGCTGGCTAACCTGTGACAAGTGT 420
Qy 421 CAGCAGAACCTATGGTCTGAGATTGTACCAACACAGCTGGCTCTGCAGCAATT 480
Db 421 CAGCAGAACCTATGGTCTGAGATTGTACCAACACAGCTGGCTCTGCAGCAATT 480
Qy 481 GCCCTGTGGGACCTTACAGGCTATGAGATGCCATAGAAATGCCATGTAGTC 540
Db 481 GCCCTGTGGGACCTTACAGGCTATGAGATGCCATAGAAATGCCATGTAGTC 540
Qy 541 AGCCATGCCATGGCCAATGATTGAGAAATTACCTTGTGCTGCC 584
Db 541 AGCCATGCCATGGCCAATGATTGAGAAATTACCTTGTGCTGCC 584
Db 541 AGCCATGCCATGGCCAATGATTGAGAAATTACCTTGTGCTGCC 584

RESULT 2
US-09-314-844F-3
Sequence 3 Application US/09314844F
Patient No. 6660839
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH CHARLES
APPLICANT: HURLE, MARK R.
APPLICANT: YOUNG, PETER
APPLICANT: TAN, K. B.
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
FILE REFERENCE: GH-50017-1
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 60/041,796
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: US 60/041,796
PRIOR FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSSQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 584
TYPE: DNA
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: UNSURE
LOCATION: (4) (10) (11) (13) (15) (38)
OTHER INFORMATION: OTHER INFORMATION: n= a, g, c or t

RESULT 3
US-09-314-844F-5
Sequence 5 Application US/09314844F
Patient No. 6660839
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH CHARLES
APPLICANT: HURLE, MARK R.
APPLICANT: YOUNG, PETER
APPLICANT: TAN, K. B.
TITLE OF INVENTION: RECEPTOR TR7
FILE REFERENCE: GH-50017-1
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 09/314,844F
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: US 60/041,796
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: US 60/041,796
PRIOR FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSSQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 588
TYPE: DNA
ORGANISM: HOMO SAPIENS
FEATURE:
NAME/KEY: UNSURE
LOCATION: (4) (10) (11) (13) (15) (38)
OTHER INFORMATION: OTHER INFORMATION: n= a, g, c or t

US-09-314-844F-3

US-09-314-844F-5

Query Match 94.2%; Score 550.2; DB 4; Length 588;
 Best Local Similarity 98.5%; Pred. No. 1.6e-128;
 Matches 572; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 1 GCGNCGGNGNGNGCAAGGTGTCAGGCCCTAGGCCCTCCCTCC 60
 Db 1 GCGNCGGNGNGCAAGGTGTCAGGCCCTAGGCCCTCCCTCC 60

Qy 61 TCTGCCGCCGTTAGCAGTGACATGGGTGAGGTAGATGGCTCCGGAG 120
 Db 61 TCTGCCGCCGTTAGCAGTGACATGGGTGAGGTAGATGGCTCCGGAG 120

Qy 121 GCGGGGTGGATGGCGTGGCGAGAACAGGGCCATTCCAGTCGCCGCC 180
 Db 121 GCGGGGTGGATGGCGTGGCGAGAACAGGGCCATTCCAGTCGCCGCC 180

Qy 181 CGGCCACCTTGCGAGTCGGGACCTTCGGAGCACGCC 240
 Db 181 CGGCCACCTTGCGAGTCGGGACCTTCGGAGCACGCC 240

Qy 241 TC-GCCTCTGCAGCCGATCGCCGCTAGCCAGATGATEGGGGCTCCCT 299
 Db 241 TC-GCCTCTGCAGCCGATCGCCGCTAGCCAGATGATEGGGGCTCCCT 300

Qy 300 CTCCCTGCTTGGATTCTTAGCACCACAGCTAGCCGAACTGGCTGAATTC 359
 Db 301 CTCCCTGCTTGGATTCTTAGCACCACAGCTAGCCGAACTGGCTGAATTC 360

Qy 360 ATTGGACATAACCCCATGTTGACCGTGTGCTAACCTGTGACAAGTGT 419
 Db 361 ATTGGACATAACCCCATGTTGACCGTGTGCTAACCTGTGACAAGTGT 420

Qy 420 CCAGAGGAACTATGTCCTGAGCATGTACCAACAGCTGGGTCTGAGCAGT 479
 Db 421 CCAGAGGAACTATGTCCTGAGCATGTACCAACAGCTGGGTCTGAGCAGT 480

Qy 480 TGCCCTGTGGGGACCTTACAGGATGAGAAATGCCATGACTGTAGT 539
 Db 481 TGCCCTGTGGGGACCTTACAGGATGAGAAATGCCATGACTGTAGT 540

Qy 540 CAGCCATGCCATGCCAATGATGAGAAATTACCTTGTCG 580
 Db 541 CAGCCATGCCATGCCAATGATGAGAAATTACCTTGTCG 581

RESULT 4
 US-09-042-785A-22
 ; Sequence 22, Application US/09042785A
 ; Patent No. 6194151

GENERAL INFORMATION:
 APPLICANT: Busfield, Samantha J
 TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LATHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042,785A
 FILING DATE: 17-MAR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/938,896

RESULT 5
 US-09-527-236A-1
 ; Sequence 1, Application US/09527236A
 ; Patent No. 6358108

GENERAL INFORMATION:
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Fan, Ping

```

; / APPLICANT: Gentz, Reiner L.
; / TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; / FILE REFERENCE: PE375P1
; / CURRENT APPLICATION NUMBER: US 09/527,236A
; / CURRENT FILING DATE: 2000-03-16
; / PRIOR APPLICATION NUMBER: 60/052,991
; / PRIOR FILING DATE: 1997-06-11
; / PRIOR APPLICATION NUMBER: 09/095,094
; / PRIOR FILING DATE: 1998-06-10
; / PRIOR APPLICATION NUMBER: 60/126,019
; / PRIOR FILING DATE: 1999-03-24
; / PRIOR APPLICATION NUMBER: 60/134,220
; / PRIOR FILING DATE: 1999-05-14
; / NUMBER OF SEQ ID NOS: 27
; / SOFTWARE: PatentIn Ver. 2.1
; / SEQ ID NO 1
; / LENGTH: 3474
; / TYPE: DNA
; / ORGANISM: Homo sapiens
; / FEATURE: CDS
; / NAME/KEY: (2211)
; / LOCATION: (247)..(2211)
; / NAME/KEY: big_peptide
; / LOCATION: (247)..(366)
; / NAME/KEY: mst_peptide
; / LOCATION: (367)..(2211)
; / US-09-527-236A-1

```

卷之三

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Db 156 GGCGGGTGGATGCGGCGCTGGGAGAAAGCAGGCCGATTCCAGTGCCTGGGCC 215

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BB 216 CCCGGCCCCCTTCCGAACTCCCCGGTTCAGCCATGGCACTTCCCAGCAGCGCCCGCCCGCC 225

2 / 3

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Qy .
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Qy 359 CATTGGCACATACCGCCATGTTGACCGTGTGCCACCGGCCAGGTAACTGTGACAAGTG 418

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479 TGGCCCTGTGGGACCTTATCCAGGCATGAGAATGCCATGACTGTAG 538

516 TTGCCCTGTGGGACCTTACAGGCATGAGAAATGCCATGACTGTAG 575
Db

Qy 539 TCAGCCATGCCCATGGCCAATTGAGAAATTACCTTGTGCTGCC 584

RESULT 6
US-09-756-854-1 Application US/09756854
; Sequence 1, Application US/09756854
; Patent No. 6667390
; GENERAL INFORMATION:
APPLICANT: Ni, Jian-Liang
; Yu, Guo-Liang
; Pan, Ping
Gent, Reiner
TITLE OF INVENTION: Human Tu
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome
STREET: 9410 Key West A
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DOS
SOFTWARE: PatentIn Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 10-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09 /
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40
REFERENCE/DOCKET NUMBER
TELECOMMUNICATION INFORMATION
TELEPHONE: 301-309-5054
TELEFAX: 301-309-8419
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 247..2211
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 367..2211
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 247..364
SEQUENCE DESCRIPTION: SEQ ID
US-09-756-854-1

Query Match 93.3%; Score
Best Local Similarity 97.4%; Prec
Matches 571; Conservative 0; N
Qy 1 GCGNCGGCGNNNGCAGGTGCA
Db 36 GCGGCCGCGCGCTGGACAGTCCAC
Qy 61 TCTGCCTGGCGTACAGTCAGTCAC
Db 96 TCTGCCGGCGGCGACAGTCAC
Qy 120 GCGGGGGTGTATGGCGTGCGATGG
Db 156 GCGGGGGTGTATGGCGTGCGATGG
Qy 180 CC-GGGCACCTTGGGAGTCCCCGGT

Db 216 CGGGGCCCTGCAAGTCCCAGTCAGGACCTCTCGAGCAGCCGC 275
 Qy 239 CCTCGCTCTCGAGCGCATCGCCAGCACAGGATGATGCGGCTCCCT 298
 Db 276 CCTCGCTCTCGAGCGCATCGCCAGCACAGGATGATCGGGCTCCCT 335
 Qy 299 TCTCTGCTGGATCTTGGACCACTTGACCAACAGCTAGCCGAACAGCTGAATCT 358
 Db 336 TCTCCCTGCTGGATCTTGGACCAACAGCTAGCCGAACAGCTGAATCT 395
 Qy 359 CATTGGCACATACCGCACATGGTACCGGCACTGGCTAACCTGTGACAAGTG 418
 Db 396 CATTGGCACATACCGCACATGGTACCGGCACTGGCTAACCTGTGACAAGTG 455
 Qy 419 TCCAGAGGGAACTTATGTCATGCTGACCATCTTACCAACACAAGCTGGCTCTCGAGCG 478
 Db 456 TCCAGAGGGAACTTATGTCATGCTGACCATCTTACCAACACAAGCTGGCTCTCGAGCG 515
 Qy 479 TTGCCCTGTGGGACTTTACAGGATGGAATGAGAATGCAATGACTGTAG 538
 Db 516 TTGCCCTGTGGGACTTTACAGGATGGAATGAGAATGCCATGACTGTAG 575
 Qy 539 TAGGCCATGCCATGCCCAATGATGAGAAATTACCTTGTGCTGCC 584
 Db 576 TAGGCCATGCCATGCCCAATGATGAGAAATTACCTTGTGCTGCC 621

RESULT 7
 US-09-042-785A-3
 Sequence 3, Application US/09042785A
 Patent No. 6194151
 GENERAL INFORMATION:
 APPLICANT: Busfield, Samantha J
 TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LATHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042-785A
 FILING DATE: 17-MAR-1998
 PRIOR APPLICATION NUMBER: US 08/938,896
 APPLICATION NUMBER: US 08/938,896
 FILING DATE: 26-SEP-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E
 REGISTRATION NUMBER: 36,207
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2612 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 190..951
 US-09-042-785A-3

Query Match 90.7%; Score 529.4; DB 3; Length 2612;
 Best Local Similarity 98.4%; Prev. No. 3.8E-123;
 Matches 555; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
 Qy 23 GCTAGGCCCTAGGCCCTCCCTGCCGCCCTCCCTGCCGGTAGCAGTGCA 82
 Db 1 GCTAGGCCCTAGGCCCTCCCTGCCGGTAGCAGTGCA 60
 Qy 83 CATGGCTTGGGTAGATGGCTCCGG-CGGGAGGGGGATGCGCGCTG 141
 Db 61 CATGGCTTGGGTAGATGGCTCCGGGGAGGGGGATGCGCGCTG 120
 Qy 142 GGCAAAGAGGAGGCCGATTCCAGCTGGCCGCC-GGCCACCTPTGCGATCCCC 200
 Db 121 GGCAAAGAGGAGGCCGATTCAGCTGGCCGCCCTGGGTCCCC 180
 Qy 201 GGTCAGCCATGGGACCTCTCCAGGAGCAGCACCCCTGCCCTCGAGCGCATC 260
 Db 181 GGTCAGCCATGGGACCTCTCCAGGAGCAGCACCCCTGCCCTCGAGCGCATC 240
 Qy 261 GCCGCCGAGGCCAAGGCCAGATAATGCCAGGAGCAGCACCCCTGCCCTCGAGCGCATC 320
 Db 241 GCCGCCGAGGCCAAGGCCAGATAATGCCAGGAGCAGCACCCCTGCCCTCGAGCGCATC 300
 Qy 321 ACCACACAGCTGAGGAGAAAGGCTGAAATGCCATACGCCATGTGTT 380
 Db 301 ACCACACAGCTGAGGAGAAAGGCTGAAATGCCATACGCCATGTGTT 360
 Qy 381 GACCGTGCACCGCCAGGTGCTAACCTGTGACAAAGTGTCCAGGAACTATGCTCT 440
 Db 361 GACCGTGCACCGCCAGGTGCTAACCTGTGACAAAGTGTCCAGGAACTATGCTCT 420
 Qy 441 GAGGATTGACCAACAGCCCTGCGCTGCGCAGSTGCCCCTGGGACCTTAC 500
 Db 421 GAGGATTGACCAACAGCCCTGCGCTGCGCAGSTGCCCCTGGGACCTTAC 480
 Qy 501 AGGCATGAGATGGATAGAAATGCCATGACTGAGCAGCATGCCATGCCAATG 560
 Db 481 AGGCATGAGATGGATAGAAATGCCATGACTGAGCAGCATGCCATGCCAATG 540
 Qy 561 ATGGAAATTACCTTGCTGCC 584
 Db 541 ATGGAAATTACCTTGCTGCC 564

RESULT 8
 US-09-042-785A-3
 Sequence 1, Application US/08959382
 Patent No. 6013176
 GENERAL INFORMATION:
 APPLICANT: DEEN, KEITH
 APPLICANT: HURLE, MARK
 APPLICANT: YOUNG, PETER
 APPLICANT: ZAN, K.B.
 TITLE OF INVENTION: Tumor Necrosis Related Receptor
 TITLE OF INVENTION: TR7
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RATNER & PRESTIA
 STREET: P.O. BOX 980
 CITY: VALLEY FORGE
 STATE: PA
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/959,382
 FILING DATE: 28-OCT-1997

CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/041,796
 FILING DATE: 02-APR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F.
 REGISTRATION NUMBER: 23 , 031
 REFERENCE/DOCKET NUMBER: GH-50017
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2186 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-959-382-1

Query Match 65.2%; Score 381; DB 3; Length 2186;
 Best Local Similarity 100.0%; Pred. No. 4 .e-86; Mismatches 0; Indels 0; Gaps 0;

Matches 381; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

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 Db 1 TCAAGCATGGGACCTTCGGAGCAGCACCCCTCGGAGGCCGATCCG 60
 QY 264 CGCGGAGCACGCCAGGATGATCGGGGTCCCTTCCTGTTGAACTTGCACC 323
 Db 61 CGCGGAGCACGCCAGGATGATCGGGGTCCCTTCCTGTTGAACTTGCACC 120
 QY 324 ACCACAGTCAGGAGAACGAGAACGAGGCTCTGAATTCGCACTACGGCAATGGTGCAC 383
 Db 121 ACCACAGTCAGGAGAACGAGAACGAGGCTCTGAATTCGCACTACGGCAATGGTGCAC 180
 QY 384 CGTGTCCACGGGCCGGTCTAACCTGTGACAGACTGTCCAGGAACTTGTCTCTGAG 443
 Db 181 CGTGTCCACGGGCCGGTCTAACCTGTGACAGACTGTCCAGGAACTTGTCTCTGAG 240
 QY 444 CATTGTACAAACAAGCTGCGCTGCGAGTGCCGCTGGGACCTTACAGG 503
 Db 241 CATTGTACAAACAAGCTGCGCTGCGAGTGCCGCTGGGACCTTACAGG 300
 QY 504 CATGAGATGGCATAGAAATGCATGACTGTGAGCCATGGCAATGATT 563
 Db 301 CATGAGATGGCATAGAAATGCATGACTGTGAGCCATGGCAATGATT 360
 QY 564 GAGAAATTACCTTGCTGCC 584
 Db 361 GAGAAATTACCTTGCTGCC 381

RESULT 10
 US-09-042-785A-6
 Sequence 6, Application US/09042785A
 Patent No. 6191151
 GENERAL INFORMATION:
 APPLICANT: Bushfield, Samantha J
 TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Laiive & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042,785A
 FILING DATE: 17-MAR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/938,896
 FILING DATE: 26-SEP-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: MEI-001CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400

RESULT 9
 US-09-314-844F-1
 Sequence 1, Application US/09314844F
 Patent No. 6660339
 GENERAL INFORMATION:
 APPLICANT: DEEN, KEITH CHARLES
 APPLICANT: HURLE, MARK R.
 APPLICANT: YOUNG, PETER
 APPLICANT: TAN, K. B.
 TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED
 FILE REFERENCE: GH-50017-1
 CURRENT APPLICATION NUMBER: US/09/314,844F
 PRIOR APPLICATION NUMBER: US 60/041,796
 PRIOR FILING DATE: 1999-05-19
 PRIOR APPLICATION NUMBER: US 60/041,796
 PRIOR FILING DATE: 1997-04-02
 PRIOR APPLICATION NUMBER: US 08/959,382
 PRIOR FILING DATE: 1997-10-28
 NUMBER OF SEQ ID NOS: 6

TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 759 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..759
 US-09-042-785A-6

Query Match 64.2%; Score 375; DB 3; Length 759;
 Best Local Similarity 100.0%; Pred. No. 1..le-84;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ATGGGAACTCTCCAGCAGCACGCCCTCGCATGGGATGCCGCCGA 269
 Qy 210 ATGGGAACTCTCCAGCAGCACGCCCTCGCATGGGATGCCGCCGA 60
 Db 270 GCCACAGCCAGTAGATGCCGGGTCCTCTCGCTGGATTCTAGCACCCA 329
 Db 61 GCCACAGCCAGTAGATGCCGGGTCCTCTCGCTGGATTCTAGCACCCA 120
 Qy 330 GCTCAGCAGAACAGAGGCCTGAAATCTCATGGCACATAACCCCATTTGACCGTCC 389
 Db 121 GCTCAGCAGAACAGAGGCCTGAAATCTCATGGCACATAACCCCATTTGACCGTCC 180
 Qy 390 ACCGCCAGGTGTAACTGTGCAAGTGTCCAGAGAACCTATGGTCTGACATGT 449
 Db 181 ACCGCCAGGTGTAACTGTGCAAGTGTCCAGAGAACCTATGGTCTGACATGT 240
 Qy 450 ACCACACAGCCCTGGCTCGATGCAAGTGTGGGACTTACCGCCATAG 509
 Db 241 ACCACACAGCCCTGGCTCGATGCAAGTGTGGGACTTACCGCCATAG 300
 Qy 510 AATGCCATAGAGAACATGCCATGACTGTAGTCAAGCTGCCATGATGAGAA 569
 Db 301 AATGCCATAGAGAACATGCCATGACTGTAGTCAAGCTGCCATGATGAGAA 360
 Qy 570 TTACCTTGCTGCC 584
 Db 361 TTACCTTGCTGCC 375

RESULT 11
 US-09-042-785A-24
 Sequence 24, Application US/09042785A
 Patent No. 6194151
 GENERAL INFORMATION:
 APPLICANT: Busfield, Samantha J
 TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LATHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042.785A
 FILING DATE: 17-MAR-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/938, 896
 FILING DATE: 26-SEP-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E
 REGISTRATION NUMBER: 36.207
 REFERENCE/DOCKET NUMBER: MEI-001CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1815 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1815
 US-09-042-785A-24

Query Match 64.2%; Score 375; DB 3; Length 1815;
 Best Local Similarity 100.0%; Pred. No. 1..3e-84;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 210 ATGGGAACTCTCCAGCAGCACGCCCTCGCATGGGATGCCGCCGA 269
 Db 1 ATGGGAACTCTCCAGCAGCACGCCCTCGCATGGGATGCCGCCGA 60
 Qy 270 GCCACAGCCAGTAGATGCCGGGTCCTCTCGCTGGATTCTAGCACCCA 329
 Db 61 GCCACAGCCAGTAGATGCCGGGTCCTCTCGCTGGATTCTAGCACCCA 120
 Qy 330 GCTCAGCAGAACAGAGGCCTGAAATCTCATGGCACATAACCCCATTTGACCGTCC 389
 Db 121 GCTCAGCAGAACAGAGGCCTGAAATCTCATGGCACATAACCCCATTTGACCGTCC 180
 Db 61 GCCACAGCCAGTAGATGCCGGGTCCTCTCGCTGGATTCTAGCACCCA 120
 Qy 390 ACCGCCAGGTGTAACTGTGCAAGTGTCCAGAGAACCTATGGTCTGACATGT 449
 Db 181 ACCGCCAGGTGTAACTGTGCAAGTGTCCAGAGAACCTATGGTCTGACATGT 240
 Qy 450 ACCACACAGCCCTGGCTCGATGCAAGTGTGGGACTTACCGCCATAG 509
 Db 241 ACCACACAGCCCTGGCTCGATGCAAGTGTGGGACTTACCGCCATAG 300
 Qy 510 AATGCCATAGAGAACATGCCATGACTGTAGTCAAGCTGCCATGATGAGAA 569
 Db 301 AATGCCATAGAGAACATGCCATGACTGTAGTCAAGCTGCCATGATGAGAA 360
 Qy 570 TTACCTTGCTGCC 584
 Db 361 TTACCTTGCTGCC 375

RESULT 12
 US-09-57-236A-8/c
 Sequence 8, Application US/09527236A
 Patent No. 6358308
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Yu, Guo Liang
 APPLICANT: Fan, Ping
 APPLICANT: Gertz, Reiner L.
 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 FILE REFERENCE: PEP75P1
 CURRENT APPLICATION NUMBER: US/09/527,236A
 CURRENT FILING DATE: 2000-03-16
 PRIOR APPLICATION NUMBER: 60/052,591
 PRIOR FILING DATE: 1997-06-11
 PRIOR APPLICATION NUMBER: 09/095,094
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/126,019
 PRIOR FILING DATE: 1999-03-24
 PRIOR APPLICATION NUMBER: 60/134,220
 PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 8
 LENGTH: 345
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-527-236A-8

Query Match 45.1%; Score 263.6; DB 3; Length 345;
 Best Local Similarity 93.3%; Pred. No. 6e-57;
 Matches 319; Conservative 0; Mismatches 19; Indels 4; Gaps 4;

US-09-756-854-B

Query Match 45.1%; Score 263.6; DB 4; Length 345;
 Best Local Similarity 93.3%; Pred. No. 6e-57;
 Matches 319; Conservative 0; Mismatches 19; Indels 4; Gaps 4;

US-09-756-854-B

Qy 239 CCTGGCCCTCTGAGCGCATGCCTGGAGCAACGGCACATGATGTCGGGGCTCTCT 298
 Db 345 CCTGGCCCTCTGAGCGCATGCCTGGAGCAACGGCACATGATGTCGGGGCTCTCT 288
 Qy 299 TCTCCCTGGATTGGATTCCCTAGACCACACAGCTCAGCCAGAACAGGCTCGAATCT 358
 Db 287 TCTCC-GCTTGGATTCCCTAGACCACACAGCTCAGCCAGAACAGGCTCGAATCT 229
 Qy 359 CATGGCACATACGGCATACGGCATACGGCATACGGCATACGGCATACGGCATACGG 418
 Db 228 CATGGCACATACGGCATACGGCATACGGCATACGGCATACGGCATACGGCATACGG 169
 Qy 419 TCCAGCAGAAACCTATGCTCTGAGCATGTGACCAACAAAGCCTGCCGTGCAAG 478
 Qy 168 TCCAGCAGAAACCTATGCTCTGAGCATGTGACCAACAAAGCCTGCCGTGCAAG 110
 Qy 479 TTGCCCTGGGACCTTTACCGGCACTGAATGGCATAGAAATCCATGACTGTAG 538
 Db 109 TTGCCCTGGGACCTTTACCGGCACTGAATGGCATAGAAATCCATGACTGTAG 50
 Qy 539 TCAGCCATGCCCATGGCAATGATTGAGAAATTACCTTGTC 580
 Db 49 TCAGCCATGCCCATGGCAATGATTGAGAAATTACCTTGTC 8

RESULT 13
 Sequence 8, Application US/09756854
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 Yu, Guo-Liang
 Pan, Ping
 Gentz, Reiner
 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: MD
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/756,854
 FILING DATE: 10-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/095,094
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoover, Kelley K.
 REGISTRATION NUMBER: 40,302
 REFERENCE/DOCKET NUMBER: P375
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 345 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-756-854-B

Query Match 45.1%; Score 263.6; DB 4; Length 345;
 Best Local Similarity 93.3%; Pred. No. 6e-57;
 Matches 319; Conservative 0; Mismatches 19; Indels 4; Gaps 4;

US-09-756-854-B

Qy 239 CCTGGCCCTCTGAGCGCATGCCTGGAGCAACGGCACATGATGTCGGGGCTCTCT 298
 Db 345 CCTGGCCCTCTGAGCGCATGCCTGGAGCAACGGCACATGATGTCGGGGCTCTCT 288
 Qy 299 TCTCCCTGGATTGGATTCCCTAGACCACACAGCTCAGCCAGAACAGGCTCGAATCT 358
 Db 287 TCTCC-GCTTGGATTCCCTAGACCACACAGCTCAGCCAGAACAGGCTCGAATCT 229
 Qy 359 CATGGCACATACGGCATACGGCATACGGCATACGGCATACGGCATACGGCATACGG 418
 Db 228 CATGGCACATACGGCATACGGCATACGGCATACGGCATACGGCATACGGCATACGG 169
 Qy 419 TCCAGCAGAAACCTATGCTCTGAGCATGTGACCAACAAAGCCTGCCGTGCAAG 478
 Db 168 TCCAGCAGAAACCTATGCTCTGAGCATGTGACCAACAAAGCCTGCCGTGCAAG 110
 Qy 479 TTGCCCTGGGACCTTTACCGGCACTGAATGGCATAGAAATCCATGACTGTAG 538
 Db 109 TTGCCCTGGGACCTTTACCGGCACTGAATGGCATAGAAATCCATGACTGTAG 50
 Qy 539 TCAGCCATGCCCATGGCAATGATTGAGAAATTACCTTGTC 580
 Db 49 TCAGCCATGCCCATGGCAATGATTGAGAAATTACCTTGTC 8

RESULT 14
 Sequence 1, Application US/09042785A
 GENERAL INFORMATION:
 APPLICANT: Busfield, Samantha J
 PATENT NO. 6194151
 GENERAL INFORMATION:
 APPLICANT: Busfield, Samantha J
 TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042,785A
 FILING DATE: 17-MAR-1998
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/938,896
 FILING DATE: 26-SEP-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragours, Amy E
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: MEI-001CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400

TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3331 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 344 .. 2065
 US-09-042-785A-1

Query Match 39.5%; Score 230.8; DB 3; Length 3331;
 Best Local Similarity 88.7%; Pred. No. 1.7e-48; Indels 0; Gaps 0;
 Matches 250; Conservative 0; Mismatches 32; Strands 1;

Qy	303	CTGGCTGATTCCTTAGCAACCAACAGCTAGCCAGAACAGAGCTCGAAATCTCATT	362
Db	191	CCGGCTGATTCCTCAGCACCATCACAGCTAACAGAACAAAGACTGTGCTCCCT	250
Qy	363	GGCACATACGCCATGTTGACCAGCTAACGGCTCGAACTGTC	422
Db	251	GGCACCTACGCCATGTTGACCGTAACTGGCAGGTGTAACCTGGCACAAGTCGCCA	310
Qy	423	GCAGGAACCTATGTCCTGCAATTGACCAACAGGCTGCGGTCTGAGGTGC	482
Db	311	GCAGGAACTGATGTCCTGAGGACTACATGAGCTGGCAGTGCAAGCTGC	370
Qy	483	CCTGTTGGGACCTTACAGGCATGAGAAATGGCATGACTGTAGTCAG	542
Db	371	CCGGCGGGACCTTACAGGCATGAGAAACGGCATAGAGATGCACTGTAGTCAG	430
Qy	543	CCATGCCATGGCCATGATTGAGAAATTACCTTGCGGCC	584
Db	431	CCATGCCATGGCCATGATTGAGAAATTACCTTGCGGCC	472

Search completed: January 8, 2005, 03:55:45
 Job time : 124 secs

RESULT 15

US-09-016-434-652
 Sequence 652, Application US/09016434

GENERAL INFORMATION:

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434

FILING DATE: HEREWITHE

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

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ALIGNMENTS						
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5: /cgn2_6_ptodata/1/pubpna/us08_pubcomb.seq.*						
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19: /cgn2_6_ptodata/1/pubpna/us11_new_pubseq.*						
20: /cgn2_6_ptodata/1/pubpna/us60_new_pubseq.*						
21: /cgn2_6_ptodata/1/pubpna/us60_pubcomb.seq.*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES					
	*					
Result No.	Score	Query Length	DB ID	Description	Software	SEQ ID NO. 3
1	578	99.0	584	17 US-10-663-157-3 Sequence 3, Appli	TYPE: DNA	LENGTH: 584
2	550.2	94.2	588	17 US-10-663-157-3 Sequence 5, Appli	ORGANISM: HOMO SAPIENS	
3	544.8	93.3	2877	9 US-09-840-795-5 Sequence 5, Appli	FEATURE: misc_feature	
4	544.8	93.3	3474	9 US-09-756-854-1 Sequence 1, Appli	NAME/KEY: misc_feature	
5	544.8	93.3	3474	13 US-10-041-574-1 Sequence 1, Appli	LOCATION: (4)..(4)	
6	544.8	93.3	3474	18 US-10-834-966-1 Sequence 1, Appli	OTHER INFORMATION: n is a, c, g, or t	
7	543.2	93.0	3534	9 US-09-978-695A-63 Sequence 63, Appli	FEATURE: misc_feature	
8	543.2	93.0	3534	9 US-09-978-695A-63 Sequence 63, Appli	NAME/KEY: misc_feature	
9	543.2	93.0	3534	9 US-09-978-697-63 Sequence 63, Appli	LOCATION: (10)..(11)	
10	543.2	93.0	3534	9 US-09-999-832A-63 Sequence 63, Appli	OTHER INFORMATION: n is a, c, g, or t	
11	543.2	93.0	3534	10 US-09-189-653 Sequence 63, Appli	FEATURE: misc_feature	
12	543.2	93.0	3534	10 US-09-978-608A-63 Sequence 63, Appli	NAME/KEY: misc_feature	

PRIOR FILING DATE: 1997-10-28
 PRIORITY APPLICATION NUMBER: US 09/314, 844
 PRIOR FILING DATE: 1999-05-19
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 5
 LENGTH: 588
 TYPE: DNA
 ORGANISM: HOMO SAPIENS
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: n is a, c, g, or t
 LOCATION: (13)..(15)
 Query Match 99.0%; Score 578; DB 17; Length 584;
 Best Local Similarity 100.0%; Pred. No. 5e-154;
 Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 b Y 1 GCGNCCGNNNGNGCAAGTGTGCTGAGGGCCCTTAGNCCTCCTGCCTCCCTCC 60
 b Y 1 GCGNCCGNNNGNGCAAGTGTGCTGAGGGCCCTAGNCCTCCTGCCTCC 60
 b 61 TCTGCCCGCCGTAGCATGGCACATGGGTGTTGAGGTAGATGGCTCCGGAG 120
 b 61 TCTGCCCGCCGTAGCATGGCACATGGGTGTTGAGGTAGATGGCTCCGGAG 120
 y Y 121 GCGGGGTGGATGGCGCTGGAGAAGAGGGCCATTCCAGTCCTCCCGGCC 180
 y Y 121 GCGGGGTGGATGGCGCTGGAGAAGAGGGCCATTCCAGTCCTCCCGGCC 180
 o o 181 CGGCCACCTTGTGAGTCCTGGGACTTCAGGATGGGACCTTCGGAGAACGCC 240
 o o 181 CGGCCACCTTGTGAGTCCTGGGACTTCAGGATGGGACCTTCGGAGAACGCC 240
 b b 241 TCGCTCTCTGGATTCCTTGGACCCACAGCTAGCCAGAACAGGCTCGAAATCTCA 300
 b b 241 TCGCTCTCTGGACCCACAGCTAGCCAGAACAGGCTCGAAATCTCA 300
 y Y 301 TCCCTCTGGATTCCTTGGACCCACAGCTAGCCAGAACAGGCTCGAAATCTCA 360
 y Y 301 TCCCTCTGGATTCCTTGGACCCACAGCTAGCCAGAACAGGCTCGAAATCTCA 360
 b b 361 TTGGCACATACCGCATTGTGACCGTGGCAACCGTGTGAAAGCTTC 420
 b b 361 TTGGCACATACCGCATTGTGACCGTGGCAACCGTGTGAAAGCTTC 420
 o o 421 CAGCAGGAACTTGTCTGAGATTGCAACACAGCTGCGTCTGAGACTT 480
 o o 421 CAGCAGGAACTTGTCTGAGATTGCAACACAGCTGCGTCTGAGACTT 480
 y Y 481 GCCCTGTGGGACCTTACAGGATGAGATGGCATAGAAATGCCATGACTGACTC 540
 o o 481 GCCCTGTGGGACCTTACAGGATGAGATGGCATAGAAATGCCATGACTGACTC 540
 y Y 541 AGCCATGCCATGGCCAATGAGATTGAGAATTACCTTGCTGCC 584
 o o 541 AGCCATGCCATGGCCAATGAGATTGAGAATTACCTTGCTGCC 584
 RESULT 2
 5..10-663-157_5
 Sequence 5, Application US/10663157
 Publication No. US20040132057A1
 GENERAL INFORMATION:
 APPLICANT: DEEN, KEITH CHARLES
 APPLICANT: HURLE, MARK R.
 APPLICANT: YOUNG, PETER
 APPLICANT: TAN, K.B.
 TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS RELATED RECEPTOR TR7
 FILE REFERENCE: SKBG-3017US2
 CURRENT APPLICATION NUMBER: US/10/663,157
 CURRENT FILING DATE: 2003-09-15
 PRIOR APPLICATION NUMBER: US 60/041,796
 PRIOR FILING DATE: 1997-04-02
 PRIOR APPLICATION NUMBER: US 60/959,382
 PRIOR FILING DATE: 1999-05-19
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: n is a, c, g, or t
 LOCATION: (13)..(15)
 Query Match 94.2%; Score 550.2; DB 17; Length 588;
 Best Local Similarity 98.5%; Pred. No. 3.9e-146;
 Matches 572; Conservative 0; Mismatches 8; Indels 1; Gaps 1
 y Qy 1 GCGNCCGNNNGNGCAAGGGTGGCTAGGCCTCCCTAGNGCCTCC 60
 y Qy 1 GCGNCCGNNNGNGCAAGGGTGGCTAGGCCTCCCTAGNGCCTCC 60
 b Qy 61 TCTGCCCGCCGTAGCATGGCACATGGGACCTTCGGAGAACGCC 120
 b Qy 61 TCTGCCCGCCGTAGCATGGCACATGGGACCTTCGGAGAACGCC 120
 y Qy 61 TCTGCCCGCCGTAGCATGGCACATGGGACCTTCGGAGAACGCC 120
 y Qy 61 TCTGCCCGCCGTAGCATGGCACATGGGACCTTCGGAGAACGCC 120
 b Qy 121 GCGGGGTGGATGGCGCTGGAGAAGAGGGCCATTCCAGTCCTCC 180
 b Qy 121 GCGGGGTGGATGGCGCTGGAGAAGAGGGCCATTCCAGTCCTCC 180
 y Qy 181 CGGCCACCTTGTGAGTCCTGGGACCTTCCGGTTCAGCCATGGAGACCTCC 240
 y Qy 181 CGGCCACCTTGTGAGTCCTGGGACCTTCCGGTTCAGCCATGGAGACCTCC 240
 b Qy 241 TC-GCCCTCTGGAGCCATGCCGGGAGAACGGCTGGCTCCCT 299
 b Qy 241 TCGCCCTCTGGAGCCATGCCGGGAGAACGGCTGGCTCCCT 300
 b Qy 300 CTCCTGTTGGATTCTTAGACCCACAGCTGGAGAACGGCTGGCTCCCT 359
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 y Qy 361 ATTGGACATACGGCGAGGCTCAAGCTGCGCACTGGCGCTGAGCTGT 420
 y Qy 420 CCAGCAGAACCTATGTCTGAGATTGACCAACAAGCTGCCGTCTGAGCTGT 479
 y Qy 421 CCAGCAGAACCTATGTCTGAGATTGACCAACAAGCTGCCGTCTGAGCTGT 480
 y Qy 480 TGCCCTGTGGGACCTTACAGGATGAGATGGCATAGAAATGCCATGACTGT 539
 y Qy 481 TGCCCTGTGGGACCTTACAGGATGAGATGGCATAGAAATGCCATGACTGT 540
 y Qy 540 CAGCAGAACCTATGTCTGAGATTGAGAAATTACCTTGCTGCC 580

RESULT 3									
IS-09-840-795-5									
Sequence 5 , Application US/09840795									
Patent No. US2010143147A1									
GENERAL INFORMATION:									
APPLICANT: Murphy, Erin B.	Mattson, Jeanine D.								
APPLICANT: Bebeque, Serge J.B.	Bates, Elizabeth Esther Mary								
APPLICANT: German, Daniel M.	Gorman, Daniel M.								
APPLICANT: Lebecque, Daniel M.									
APPLICANT: Lebecque, Serge J.B.									
TITLE OF INVENTION: Mammalian Genes ; Related Reagents									
FILE REFERENCE: SF0818K									
CURRENT APPLICATION NUMBER: US/09/840,795									
CURRENT FILING DATE: 2001-04-23									
PRIOR APPLICATION NUMBER: US/09/351,777									
PRIOR FILING DATE: 1999-07-12									
NUMBER OF SEQ ID NOS: 19									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO 5									
LENGTH: 2877									
TYPE: DNA									
ORGANISM: primate									
FEATURE: CDS									
NAME/KEY: CDS									
LOCATION: (410) .. (2374)									
NAME/KEY: mat_peptide									
LOCATION: (533) .. (2374)									
S-09-840-795-5									
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Best Local Similarity	97.4%	Pred. No. 1..144;							
Matches 571; Conservative	0;	Mismatches 13;	Indels						
Y Y	1	GCGNCGGCNGNGCAAGGTGCTAGGCCCTTGAAGGTGATGGCTCCCTAGNGCTCTCC							
b b	199	GCGGCAGCCGCTGGCAGGTGCTAGGCCCTTGAAGGTGATGGCTCCCTAGNGCTCTCC							
Y Y	61	TCTGCCCTCCGCTGAGCACTGGCTTGAAGGTGATGGCTCCCTAGNGCTCTCC							
b b	259	TCTGCCCTCCGCTGAGCACTGGCTTGAAGGTGATGGCTCCCTAGNGCTCTCC							
Y Y	120	GCGGGCGTTGGATCGGCCCTGGGAAAGACGCCGGCATTCGCCATGGGATAGCTCC							
b b	319	GCGGGCGTTGGATCGGCCCTGGGAAAGACGCCGGCATTCGCCATGGGATAGCTCC							
Y Y	180	CC-GGCCAACCTTGGAGTCCCCTGGAGATGGGACCTCTCC							
b b	379	CCGGGGCCCTGGAGTCCCCTGGAGATGGGACCTCTCC							
Y Y	239	CCCTGCCTCTCTGGAGCCGCAATGCCGGAGCCAGGCCAGGATGGGATAGCTCC							
b b	439	CCRGCTCTGGAGCCGCAATGCCGGAGCCAGGCCAGGATGGGATAGCTCC							
Y Y	299	TCTCTCTGGATTCTTAGCACCAACCAGCTGCCAGAACACAGCTCC							
b b	499	TCTCTCTGGATTCTTAGCACCAACCAGCTGCCAGAACACAGCTCC							
Y Y	359	CATTGGCACATACCGCGATGTTGACCTGGCCACCGGCAAGGTGCT							
b b	559	CATTGGCACATACCGCGATGTTGACCTGGCCACCGGCAAGGTGCT							
Y Y	419	TCCAGCGAGAACCTATGCTCTGAGGATTGACCAACACAGCTCC							
b b	619	TCCAGCGAGAACCTATGCTCTGAGGATTGACCAACACAGCTCC							
Y Y	479	TTCGCCCCCTGGGGACCTTTACCGGCAATGAGAATGCTGCCAGGCT							
b b	679	TTCGCCCCCTGGGGACCTTTACCGGCAATGAGAATGCTGCCAGGCT							
Y Y	519	TGCGCCATGCCATGGCCATGATGAGAATTACCTTGCTGCTGCCAGGCT							

RESULT 4

US-09-756-854-1 Sequence 1, Application US / 09756854
 Patent No. US20020164684A1
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 Yu, Guo-Liang
 Fan, Ping
 Gantz, Reiner
 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: MD
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 09/756,854
 FILING DATE: 10-Jan-2001
 CLASSIFICATION: <Unknown>
 PRIORITY DATA:
 APPLICATION NUMBER: 09/095,094
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hoover, Kenley K.
 REGISTRATION NUMBER: 40,302
 REFERENCE/DOCKET NUMBER: PF375
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3474 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 247..2211
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 367..2211
 FEATURE:
 NAME/KEY: B19_peptide
 LOCATION: 247..364
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-756-854-1

Query Match 93.3%; Score 544.8; DB 9; Length 3474;
 Best Local Similarity 97.4%; Pred. No. 1.Se-144;
 Matches 571; Conservative 0; Mismatches 13; Indels 2;

Qy 1 GCGNCGGGNNNGNCAGGGCTTACATGGGCTTCGCGCCGCT
 Db 36 GCGcGCCCGGTGGCAGGGTGGGGCCCTAGACCTTCGCGCCG
 Qy 61 TCAGCCGCCGCTAGCACTGGGCTTAGATGGCTCCGG-C
 Db 96 TCCTCCGCCGCAGCTGGGGCTGGGGAGAGCAGGGCCTGGGG
 Qy 120 GGCGGGGTGATGGGGCTGGGGAGAGCAGGGCCTGGGG

RESULT 5

US-10-041-574-1
 CURRENT APPLICATION NUMBER: US/10/041,574
 Sequence 1, Application US/10041574
 Publication No. US20020168359A1
 GENERAL INFORMATION:
 APPLICANT: Yu, Jian
 APPLICANT: Fan, Ping
 APPLICANT: Genthz, Reiner L.
 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 FILE REFERENCE: PEP375P1

PRIOR APPLICATION NUMBER: 09/527,236
 PRIOR FILING DATE: 2000-03-16
 PRIOR APPLICATION NUMBER: 60/052,991
 PRIOR FILING DATE: 1997-06-11
 PRIOR APPLICATION NUMBER: 09/095,094
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/126,019
 PRIOR FILING DATE: 1999-03-24
 PRIOR APPLICATION NUMBER: 60/134,220
 PRIOR FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1
 LENGTH: 3474
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (247)..(2211)
 NAME/KEY: big_peptide
 LOCATION: (247)..(366)
 NAME/KEY: mat_peptide
 LOCATION: (367)..(2211)

Query Match 93.3%; Score 544.8; DB 13; Length 3474;
 Best Local Similarity 97.4%; Pred. No. 1..6e-14;
 Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

RESULT 6

US-10-034-966-1
 Sequence 1, Application US/10834966
 Publication No. US20040197870A1
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Fan, Ping
 APPLICANT: Genthz, Reiner L.
 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 FILE REFERENCE: PEP375P1
 CURRENT APPLICATION NUMBER: US/10/834,966
 CURRENT FILING DATE: 2004-04-30
 PRIOR APPLICATION NUMBER: US/10/041,574
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: 09/527,236
 PRIOR FILING DATE: 2000-03-16
 PRIOR APPLICATION NUMBER: 60/052,991
 PRIOR FILING DATE: 1997-06-11
 PRIOR APPLICATION NUMBER: 09/095,094
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/126,019
 PRIOR FILING DATE: 1999-03-24
 PRIOR APPLICATION NUMBER: 60/134,220
 PRIOR FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1
 LENGTH: 3474
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (247)..(2211)
 NAME/KEY: big_peptide
 LOCATION: (247)..(366)
 NAME/KEY: mat_peptide
 LOCATION: (367)..(2211)

Query Match 93.3%; Score 544.8; DB 13; Length 3474;
 Best Local Similarity 97.4%; Pred. No. 1..6e-14;
 Matches 571; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

FEATURE: NAME/KEY: CDS
 LOCATION: (247)..(2211)
 FEATURE: NAME/KEY: big_peptide
 LOCATION: (247)..(366)
 FEATURE: NAME/KEY: mat_peptide
 LOCATION: (367)..(2211)
 IS-10-834-966-1

	Query Match	Best Local Similarity	Score	Pred.	No.	Length
Matches	571; Conservative	97.4%	DB 18;	DB 18;	Length	3474;
	0; Mismatches	13;				
	Indels	2;				
	Gaps	2;				
Dy	1 GCGNCCGNNINGAAGGTGCTAGGCGCCCTTNGNCCTCCCTGGCCCTCCTCC 60	93.3%	Score	544.8;	DB 18;	Length 3474;
Dy	36 GCGGCCGCCCCCTGGCAGGTGCTAGGCCTCCCTGGCCCTCCTCC 95					
Dy	61 TCTGCCGGCCTAGAGTGACATGGGTGTTGGAGTAGATGGCTCCGGCGGG 119					
Dy	96 TCTGCCGGCAGAGTGTGACATGGGTGTTGGAGTAGATGGCTCCGGCGGG 155					
Dy	120 GCGGGCGGTGGATGGCCGGCTGGGACAAGCAGCCGATTCAGCTGGCCGGCC 179					
Dy	156 GCGGCCGTTGGATGGCCGGCTGGAGCAAGCAGCTGGCCGGCC 215					
Dy	180 CC-GGCCACCTTGGAGTCCCCTGAGCATGGGACTCTCCAGAACGAGCCG 238					
Dy	216 CGGGGCCCCCTGGAGTCCCCTGAGCATGGGACTCTCCAGAACGAGCCG 275					
Dy	239 CCTGGCTCTGGGATTCAGGGCATGGCCAGCAAGCCAAGGCCAGTGAATCGGGGCTCCCT 298					
Dy	276 CCTGGCTCTGGGATTCAGGGCATGGCCAGCAAGCCAAGGCCAGTGAATCGGGGCTCCCT 335					
Dy	299 TCTCTGCTGGATTCTAGCACACACAGCTAGCCAAACAGAAAGGCTCGAACT 358					
Dy	336 TCTCTGCTGGATTCTAGCACACACAGCTAGCCAAACAGAAAGGCTCGAACT 395					
Dy	359 CATGGGACATACGGCAATGTGACCGCCAGTGTGCACTGTGAACTGTG 418					
Dy	396 CATGGGACATACGGCAATGTGACCGCCAGTGTGCACTGTGAACTGTG 455					
Dy	419 TCCAGGAGAACCTATGCTCTGAGATTGACATGAGCTGGCTCGAGCAG 478					
Dy	456 TCCAGGAGAACCTATGCTCTGAGATTGACATGAGCTGGCTCGAGCAG 515					
Dy	479 TTGCCCCATGGGACACCTTAACAGGATGAGAAATGCATGAGAAATGCCATGCTGTG 538					
Dy	516 TTGCCCCATGGGACACCTTAACAGGATGAGAAATGCATGCTGTG 575					
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RESULT 7

IS-09-978-295A-63
 Sequence 63, Application US/09978295A
 General Information:
 Parent No. US0020156065A1
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Geritsen, Audrey E.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Sheldon, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P2630PC11
 CURRENT APPLICATION NUMBER: US/09/978,295A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
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; PRIORITY APPLICATION NUMBER: 60/085574
; PRIORITY FILING DATE: 1998-05-15
; PRIORITY APPLICATION NUMBER: 60/085697

Query Match 93 %; Score 543.2; DB 9; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.4e-14;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

Qy 1 GCGNCCGGNNNGCAAGGGTGTGAGGCCCTAGNGCCTCCCTGCCGCTCCCTC 60
Db 114 GCGCCCTGCCCTGGCAGGTGTGAGGCCCTAGAGCTCCTGCCGCTCCCTC 173
Qy 61 TCTGCCCCGGCGTAGCGTGCACATGGGTGTTGGAGTAGATGGGTGATGGGG -CGGGGA 119
Db 174 TCTGCCCCGGCGTAGCGTGCACATGGGTGTTGGAGTAGATGGGTGATGGGG -CGGGGA 233
Qy 120 GGGGCGGTGGATGGCGGATGGCGATGGCGATGGCGATGGCGATGGCG 179
Db 234 GGGGGCGGTGGATGGCGGATGGCGATGGCGATGGCGATGGCGATGGCG 293
Qy 180 CC-GCCACCCCTGGAGTCCCCGGTCAGCCATGGGACCTCTCGAGGAGCACGC 238
Db 294 CGCGCCCTCTGGCATGGGACCTCTCGAGGAGCACGCACCG 353
Qy 239 CCTCGCCCTCCTCGAGCCATGGGACCTCTCGAGGAGCACGCACCG 298
Db 354 CCTCGCCCTCTGGCATGGGACCTCTCGAGGAGCACGCACCG 413
Qy 299 TCTCTGCTGGATCTGAGCTTGGATCTGAGCTGGCTCTGAGACTCT 358
Db 414 TCTCTGCTGGATCTGAGCTTGGATCTGAGCTGGCTCTGAGACTCT 473
Qy 359 CATTGGACATACGCCATGGTGAAGCTGGCTGCCACGCCACGCCACGCC 418
Db 474 CATTGGACATACGCCATGGTGAAGCTGGCTGCCACGCCACGCCACGCC 533
Qy 419 TCCAGGAGAACCTATGCTCTGAGCTTGGACACACAAGCTGGGCTGGAGCAG 478

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RESULT 8

US-09-978-6-97-63
 Sequence 63, Application US/09978697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey E.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kliavkin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Naper, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2630P1C27

CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03

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 PRIOR FILING DATE: 1997-11-13

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 PRIOR FILING DATE: 1998-03-31

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 PRIOR FILING DATE: 1998-03-31

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 PRIOR FILING DATE: 1998-03-31

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 PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01

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 PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080338
 PRIOR FILING DATE: 1998-04-08

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 PRIOR FILING DATE: 1998-04-09

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 PRIOR FILING DATE: 1998-04-09

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 PRIOR FILING DATE: 1998-04-15

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 PRIOR FILING DATE: 1998-04-15

PRIOR APPLICATION NUMBER: 60/081838
 PRIOR FILING DATE: 1998-04-22

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 PRIOR FILING DATE: 1998-04-22

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 PRIOR FILING DATE: 1998-04-22

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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

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 Qy 61 TCGGCCGCGCTAGATGCACTGGGTTGGAGTAGTGGGTCCCG-CCCGGA 119
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 Qy 120 CGCGCGCTGGATGCGCGCTGGAGAAGCAGCCGCATTCAGCTGCCCGGGCC 179
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 Qy 180 CC-GGCCACCTTGCASTCCCGGTTCAAGGCGACTCTCCAGCACCCGC 353
 Db 294 CGCGCGCCCTGGAGCTCCGGTCAAGCAGCGATGGGAACTCTCCAGCACCGC 353
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.0%; Score 543.2; DB 9; Length 3534;
 Best Local Similarity 97.3%; Pred. No. 4.4e-14;
 Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

RESULT 9
 US-09-978-192A-63
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 ; Patent No. US2002017755A1
 ; GENERAL INFORMATION:
 / APPLICANT: Abkenazi, Avi
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Batton, Dan
 / APPLICANT: Ferrara, Napoleon
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerber, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Hillian, Kenneth J.
 / APPLICANT: Klijavin, Ivar J.
 / APPLICANT: Kuo, Sophia S.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Shelton, David L.
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel P.
 / APPLICANT: Williams, P. Mickey
 / APPLICANT:

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US10/978,19A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/919585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085697

Query Match Score 543.2; DB 9; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4-4e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William J.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2630PLIC63
CURRENT APPLICATION NUMBER: US/09/999, 832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/91885
PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.0%; Score 543.2%; DB 9; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.4e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 8 2; Gaps 2;

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Db 114 GCGGCCTCGCGCTCGAGCTCCCTGCGCCCTCCCTGCGCC 173
QY 61 TCTGCCCGGGCGTAGAGTCACATGGGTGGATGGCTGGGA 119
Db 174 TCTGCCGGCGCACGTCACATGGGTGGATGGCTGGGA 233
QY 120 CGCGGGGGATGGCTGGCGCTGGGAGAAGCAGGGGATGGCTGGGG 179
Db 234 GCGGGGGATGGCTGGCGCTGGGAGAAGCAGGGGATGGCTGGGG 293
QY 180 CC-GCCACCATTTGCGAAGTCCCCTGCGAGCAGCACCGC 238
Db 294 CGGGGGCCCCCTGCGAGTCCCCTGCGAGCAGCACCGC 353

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QY 239 CCTCCCTCCCTGCAGCGATGCCAACAGCCACGATGATCGGGGCTCCCT 298
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 QY 299 TCTCCTGTTGGATTCTTACGACCACAGCTCAAGAACAGGCTCGAATCT 358
 Db 414 TCTCCTGTTGGATTCCTAGCACACAGCTCAAGAACAGGCTCGAATCT 473
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 QY 479 TTGCCCTGTTGGACCTTACAGGGCATGAAATGGCATAGAGAAATGCCATGTAG 538
 Db 594 TTGCCCTGTTGGACCTTACAGGCATGAAATGCCATGTAGAAATGCCATGTAG 653
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 Db 654 TCAGCATGCCATGCCATGCCATGCAATGATGAAATAATTACCTTGCMGCC 699

RESULT 11
 US-09-978-189 63
 Sequence 63, Application US/09978189
 Publication No. US20030004102A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filivroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
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 APPLICANT: Pai, James
 APPLICANT: Paoni, Nicholas F.
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 APPLICANT: Shalton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William J.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 CURRENT APPLICATION NUMBER: US/09/978,189
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match Score 543.2; DB 10;
Best Local Similarity 97.0%; Prod. No. 4.4e-14;
Matches 570; Mismatches 0; Indels 2; Gaps 2;
Qy 1 GCGCCGCGNNNNNGCAAGGTCTGACGCCCTAGNCCTCCCTGGCCCTCCCTGC 60
Db 114 GCGCCCTCCCGCTGGAGGTCTGACGCCCTAGNCCTCCCTGGCCCTCCCT 173
Qy 61 TCGCCCGCCGCTGAGACTGCACTGGGGTGTGGAGTAGTGGAATGGGGAA 119
Db 174 TCGCCCGCCGAGCTGCACTGGGGTGTGGAGTAGTGGAATGGGGAA 233
Qy 120 GCGCCGGTGGATCGGGCTGGAGCACAGCAGGGATTCAAGCTGGCCGCC 179
Db 234 GCGCCGGTGGATCGGGCTGGAGCACAGCAGGGATTCAAGCTGGCCGCC 293
Qy 180 CC-CGCCACCTTGGAGTCGCCGTTCAAGCATGGGACCTCTCGAGCACCCC 238
Db 294 CCGGGCCGCCCTGGAGTGGCCCGGTTCAAGCATGGGACCTCTCGAGCACCCC 353
Qy 239 CCTGGCCCTCTGAGGCCGATGCCCGCAGGCAAGCTGATGGACCTCTCGAGCACCCC 298
Db 354 CCTGGCCCTCTGAGGCCGATGCCCGCAGGCAAGCTGATGGACCTCTCGAGCACCCC 413
Qy 299 TCTCTGCTGGATTCCTAGCACCCAGCTAGCCAGAACAGAAGGGCTGTAATCT 358
Db 414 TCTCTGCTGGATTCCTAGCACCCAGCTAGCCAGAACAGAAGGGCTGTAATCT 473
Qy 359 CATGGCACATAAGCCATGGTGAAGGTGGTAACCTGTGAAAGTGC 418
Db 474 CATGGCACATAAGCCATGGTGAAGGTGGTAACCTGTGAAAGTGC 533
Qy 419 TCCAGCAGAACCTATGCTCTGAGTACCAACACAAGCTGGGGTCTCAGCAG 478
Db 534 TCCAGCAGAACCTATGCTCTGAGTACCAACACAAGCTGGGGTCTCAGCAG 593
Qy 479 TTGGCCCTGGGGACCTTACCAAGCATGAGAATGGCAATAGAAAATGCCATGGCTGTAG 538
Db 594 TTGGCCCTGGGGACCTTACCAAGCATGAGAATGGCAATAGAAAATGCCATGGCTGTAG 653
Qy 539 TCAAGCATGCCCATGGCAATGCAATGATTGAGAAATACCTTGTGCC 584
Db 654 TCAAGCATGCCCATGGCAATGCAATGATTGAGAAATACCTTGTGCC 699

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RESULT 12

US-09-918-608A-63

Sequence 63, Application US/0978608A

; Publication No. US2003004462A1

; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bobstein, David
; APPLICANT: Denoyers, Luc
; APPLICANT: Bacon, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hans Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

1 APPLICANT: Grimaldi, J. Christopher
 1 APPLICANT: Gurney, Austin L.
 1 APPLICANT: Hillian, Kenneth J.
 1 APPLICANT: Kljavin, Ivar J.
 1 APPLICANT: Kuo, Sophia S.
 1 APPLICANT: Napior, Mary A.
 1 APPLICANT: Pan, James;
 1 APPLICANT: Paoni, Nicholas F.
 1 APPLICANT: Roy, Margaret Ann
 1 APPLICANT: Shelton, David L.
 1 APPLICANT: Stewart, Timothy A.
 1 APPLICANT: Tumas, Daniel
 1 APPLICANT: Williams, P. Mickey
 1 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P26-0P1C22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 63
LENGTH: 3534
TYPE: DNA
ORGANISM: Homo sapiens
US-09-978-608A-63

Query Match 93.0%; Score 543; DB 10; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGNCCGGNNNGCAAGGTGCTGAGGCCCTAGNCCTCCCTGCCCTCCCTCC 60
Db 114 GCGGCCCTCGCGCTGGCGAGGTGCTGAGGCCCTTAGACCTCCCTGCCCTCC 173
QY 61 TCTGCCTGGCGTGTAGCATGGTCACATGGGTGTTGGAGGTAGATGGCTCCCGG-CCTGGA 119
Db 174 TCTGCCCGCCGCGCACATGGGTGTTGGAGTGGTAGATGGCTCCGacccGGA 233
QY 120 GCGCGCGTGGATCGGGCTGGCGAGCAAGGAGCAGCGCCATTCAACATGGGACTCTCGAGAGCAGCGCC 179
Db 234 GCGCGCGTGGATCGGGCTGGCGAGCAAGGAGCAGCGCCATTCAACGTCGGCCACCC 293
QY 180 CC-GGCCACCTGGAGTCCCGGTTCAACCATGGGACTCTCGAGAGCAGCGC 238
Db 294 CCGCGGCCCTCTGGAGTCCCGGTTCAACCATGGGACTCTCGAGAGCAGCGC 353
QY 239 CCTTGCCATCTGAGCCGATCGCCGGAGCATGGCTAACCTGTACAAGTG 473
Db 354 CCTGGCCATCTGAGCCGATCGCCGGAGCATGGCTAACCTGTACAAGTG 413
QY 299 TCTCTGCTGGATTCTGAGCCACAGCTTACGGCTAGTGTACGGCTCC 358
Db 414 TCTCTGCTGGATTCTGAGCCACAGCTTACGGCTAGTGTACGGCTCC 473
QY 359 CATTGGCACATACGGCATGGCTAGTGTACGGCTAGTGTACGGCTCC 418
Db 474 CATTGGCACATACGGCATGGCTAGTGTACGGCTAGTGTACGGCTCC 533
QY 419 TCCAGCAGAAACCTATGGCTGAGCATGGTACAAACAGAGCTGGGGTCTGAGGGAG 478
Db 534 TCCAGCAGAAACCTATGGCTGAGCATGGTACAAACAGAGCTGGGGTCTGAGGGAG 593
QY 479 TTGCCCTGGGGACCTTACGGCATGGCTGAGCATGGTACAAATGGCTGAG 538
Db 594 TTGCCCTGGGGACCTTACGGCATGGCTGAGCATGGTACAAATGGCTGAG 653
QY 539 TCAGCCATGCCCATGGCAATGTTGAGAATAACCTGTGCTGCC 584
Db 654 TCAGCCATGCCCATGGCAATGTTGAGAATAACCTGTGCTGCC 699

Query Match 93.0%; Score 543.2%; DB 10; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGNCCGGNNNGCAAGGTGCTGAGGCCCTAGNCCTCCCTGCCCTCC 60
Db 114 GCGGCCCTCGCGCTGGCGAGGTGCTGAGGCCCTAGACCTCCCTGCCCTCC 173
QY 61 TCTGCCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 119
Db 174 TCTGCCCGCCGCAAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 233
QY 120 GCGCGCGTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 179
Db 234 GGGCGCCCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 293
QY 180 CC-GGCCACCTGGGACTCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 353
Db 294 CCGCGGCCCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 353
QY 299 CCTGGCTCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 298
Db 354 CCTGGCTCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 413
QY 299 TCTCTGCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 358
Db 414 TCTCTGCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 473
QY 539 TCAGCCATGCCCATGGCAATGTTGAGAATAACCTGTGCTGCC 584
Db 654 TCAGCCATGCCCATGGCAATGTTGAGAATAACCTGTGCTGCC 699

Query Match 93.0%; Score 543.2%; DB 10; Length 3534;
Best Local Similarity 97.3%; Pred. No. 4.e-144;
Matches 570; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 1 GCGNCCGGNNNGCAAGGTGCTGAGGCCCTAGNCCTCCCTGCCCTCC 60
Db 114 GCGGCCCTCGCGCTGGCGAGGTGCTGAGGCCCTAGACCTCCCTGCCCTCC 173
QY 61 TCTGCCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 119
Db 174 TCTGCCCGCCGCAAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 233
QY 120 GCGCGCGTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 179
Db 234 GGGCGCCCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 293
QY 180 CC-GGCCACCTGGGACTCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 353
Db 294 CCGCGGCCCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 353
QY 299 CCTGGCTCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 298
Db 354 CCTGGCTCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 413
QY 299 TCTCTGCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 358
Db 414 TCTCTGCTGGATGGCTGGAGCTGGCTGGAGCTGGCTGGAGCTGGCTGGAG 473
QY 539 TCAGCCATGCCCATGGCAATGTTGAGAATAACCTGTGCTGCC 584
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RESULT 14

US-09-978-191A-63

Sequence 63, Application US/09978191A

Publication No. US20030050239A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Klijavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napior, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P2630P1C4

CURRENT APPLICATION NUMBER: US/09/978,191A
 PRIOR APPLICATION NUMBER: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/948585
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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query	Match	Score	Length
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Best Local Matches	97.3%	Pred. No. 4.4e-144;	
Matches	570;	Mismatches 14;	
	0;	Indels 2;	
		Gaps 2;	
Qy	1	GCCNCCGGNNNGCAAGGTGCTGAGGCCCTACNGCCTCCCTGCCCTCC 60	
Db	114	GCCTCGCCCTGGGAGGTGAGGCCCTAGGCCCTCTGCCCTCC 173	
Qy	61	TCTGCCGGCGTAGAGTCACATGGGTCTGGAGTAGTGGGTCTCCGGGA-CGGGA 119	
Db	174	TCTGCCGGCGCAGAGTCACATGGGTCTGGAGTAGTGGGTCTCCGGGA 233	
Qy	120	GGGGCGGTGGATGGCGCTGGACAAGAGCGCTGGATTCAGTGCCCCGGGCC 179	
Db	234	GCGCGCTGGATGCCGGCGAGGGCGATTCAGTGCCCCGGGCC 293	
Qy	180	CC-GCCACCTTGCAGTCAGATGGGACCTCTCGAGCAGCACCGC 238	
Db	294	CCTGGGCCCTGAGTCCGGGACCTCTCGAGCAGAACGAGCACCGC 353	
Qy	239	CTTCGCTTCCTGAGGCCATGCCGCGAGCCAGCCACGATGATCGCTGGCTCCCT 298	
Db	354	CTTCGCTTCCTGAGGCCATGCCGCTGGCTCCCT 413	
Qy	299	TCTCTCTTGTGATCTTGGACACCAAGCTGGAGAAGGGCTCTGAATCT 358	
Db	414	TCTCTGTGTTGATCTTGGACACCAAGCTGGAGAAGGGCTCTGAATCT 473	
Qy	359	CATTGGCACATACGCCATGGTGAACCTGCACTGTGACAGTG 418	
Db	474	CATTGGCACATACGCCATGGTGAACCTGCACTGTGACAGTG 533	
Qy	419	TCCAGGAAACCTATGTTCTGAGCATTTGACCAACACAACCTGGCGTCTGACAG 478	
Db	534	TCCAGGAAACCTATGTTCTGAGCATTTGACCAACACAACCTGGCGTCTGACAG 593	
Qy	479	TGCGCCGTGGGACCTTACAGGATGAGAATGGCATGAGAAATGCCATGACTGTG 538	
Db	594	TGCGCCGTGGGACCTTACAGGATGAGAATGGCATGAGAAATGCCATGACTGTG 653	
Qy	539	TGAGCCATGCCATGGCAATGATGAGAAATTACCTGTGTGCC 584	
Db	654	TGAGCCATGCCATGGCAATGAGAAATTACCTGTGTGCC 699	

RESULT 15

US-09-978-403A-63
 ; Sequence 63, Application US/09978403A
 ; Publication No. US20030050240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hans Peter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurley, Austin L.
 ; APPLICANT: Hillman, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Naper, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.

```

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630B1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 09/18585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
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Search completed: January 8, 2005, 05:20:09
 Job time : 575 secs

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Query Match          93.0% Score 543.2; DB 110; Length 3534;
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Qy     120 GCGGGCGGTGATGCGCGCTGGGAGAAGAGCGCCGATTCAGCTGGCTCC 179
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